



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 108250

TO: Elizabeth Kemmerer
Location: cm1/10b17/10d19
Art Unit: 1646
Sunday, November 16, 2003

Case Serial Number: 08/741095

From: Toby Port
Location: Biotech-Chem Library
CM1-6A04
Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Kemmerer,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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W096/34095


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DB      181 HOTKCSMLVTKAGAGSSSHWMMWFLSGSLVIVYVSTGLIICVRRKRPBGDVVIVIS 240
QY      241 VORKROEAGEATVIEALQAPPDVTTVAVEETIPSTGSPNH 283
DB      241 VORKROEAGEATVIEALQAPPDVTTVAVEETIPSTGSPNH 283

RESULT 2
US-09-934-289A-13
; Sequence 13, Application US/09934289A
; Patent No. US20020132297A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: M81098-061C1C1(M)
; CURRENT APPLICATION NUMBER: US/09/934,289A
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/342,767
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/146,950
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: (1)...(38)
US-09-934-289A-13

Query Match      100.0%; Score 1578; DB 10; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.7e-126;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MEBPGWGPMPWRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDYVPGSECCPKCSPG 60
DB      1 MEBPGWGPMPWRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDYVPGSECCPKCSPG 60
QY      61 YRKEACGELTGTVCPCPGTYIAHLNGLSKLQCDPAMGLRASNCSTRTENAVCG 120
DB      61 YRKEACGELTGTVCPCPGTYIAHLNGLSKLQCDPAMGLRASNCSTRTENAVCG 120
QY      121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLQNCPCPGTSPNGTLEECQ 180
DB      121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLQNCPCPGTSPNGTLEECQ 180
QY      181 HOTKCSMLVTKAGAGTSSSHWMMWFLSGSLVIVYVSTGLIICVRRKRPBGDVVIVIS 240
DB      181 HOTKCSMLVTKAGAGTSSSHWMMWFLSGSLVIVYVSTGLIICVRRKRPBGDVVIVIS 240
QY      241 VORKROEAGEATVIEALQAPPDVTTVAVEETIPSTGSPNH 283
DB      241 VORKROEAGEATVIEALQAPPDVTTVAVEETIPSTGSPNH 283

RESULT 3
US-09-935-727-31
; Sequence 31, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
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QY      1 MEBPGWGPMPWRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDYVPGSECCPKCSPG 60
DB      1 MEBPGWGPMPWRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDYVPGSECCPKCSPG 60
QY      61 YRKEACGELTGTVCPCPGTYIAHLNGLSKLQCDPAMGLRASNCSTRTENAVCG 120
DB      61 YRKEACGELTGTVCPCPGTYIAHLNGLSKLQCDPAMGLRASNCSTRTENAVCG 120
QY      121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLQNCPCPGTSPNGTLEECQ 180
DB      121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLQNCPCPGTSPNGTLEECQ 180
QY      181 HOTKCSMLVTKAGAGTSSSHWMMWFLSGSLVIVYVSTGLIICVRRKRPBGDVVIVIS 240
DB      181 HOTKCSMLVTKAGAGTSSSHWMMWFLSGSLVIVYVSTGLIICVRRKRPBGDVVIVIS 240
QY      241 VORKROEAGEATVIEALQAPPDVTTVAVEETIPSTGSPNH 283
DB      241 VORKROEAGEATVIEALQAPPDVTTVAVEETIPSTGSPNH 283

RESULT 4
US-10-020-787-2
; Sequence 2, Application US/10020787
; Publication No. US20020102258A1
; GENERAL INFORMATION:
; APPLICANT: Hartop, Jeremy A.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Reddy, Manjula P.
; APPLICANT: Truneh, Alemsseged
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-Like 2 (TLR2) Antibodies
; FILE REFERENCE: GH50027C1
; CURRENT APPLICATION NUMBER: US/10/020,787
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 09/403,815
; PRIOR FILING DATE: 1999-10-26
; PRIOR APPLICATION NUMBER: PCT/US98/09744
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/046,249
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	Query Match	68.0%	Score 1073	DB 103	Length 419
	Best Local Similarity	100.0%	Pred. No. 7.2e-83		
	Matches 185	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MEPPGDWGPMPWRSTPRDVLRLVLYTFLGAPCAPALPSCKEDEYPVGSECCPKCSBG	60		
Dd	1	MEPPGDWGPMPWRSTPRDVLRLVLYTFLGAPCAPALPSCKEDEYPVGSSCCPKCSBG	60		
Qy	61	YRVBACGLGTGVCEPCPGFTYIAHLNGLSCLCQCOCDDPMGLRASNCRTENAVCG	120		
Dd	61	YRVBACGLGTGVCEPCPGFTYIAHLNGLSCLCQCOCDDPMGLRASNCRTENAVCG	120		
Qy	121	CSPGHFCIVODGDHCACAGPAVTSSPGQRVQKGTESODTLCONCPPTGFSPNGTLEBCQ	180		

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1 RESULT 10
2 US-09-934-289A-18
3 : Sequence 18, Application US/09934289A
4 : Patent No. US20020132297A1
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: Busfield, Samantha J.
9 :
10 : TITLE OF INVENTION: NOVEL MOLECULES OF THE
11 :
12 : TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
13 :
14 : TITLE OF INVENTION: PROTEIN FAMILY AND USBS THEREOF
15 :
16 : FILE REFERENCE: MBIO98-06(CIPAC1(M)
17 :
18 : CURRENT APPLICATION NUMBER: US/09/934,289A
19 :
20 : PRIOR FILING DATE: 2001-08-21
21 :
22 : PRIOR APPLICATION NUMBER: US 09/342,767
23 :
24 : PRIOR FILING DATE: 1998-06-29
25 :
26 : PRIOR APPLICATION NUMBER: US 09/146,950
27 :
28 : PRIOR FILING DATE: 1998-09-03
29 :
30 : NUMBER OF SEQ ID NOS: 58
31 :
32 : SOFTWARE: FastSeq for Windows Version 3.0

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;; PRIOR FILING DATE: 1997-05-12
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 283
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-10-020-787-2

Query Match 99.8%; Score 1575; DB 14; Length 283;
Best Local Similarity 99.6%; Pred. No. 1.4e-125;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMSTPRTDVLRLVLYLTFIAGPCYAPALPSCKEDEYVSGCCPKCSPG 60
DB 1 MEPPGDMGPPPMSTPRTDVLRLVLYLTFIAGPCYAPALPSCKEDEYVSGCCPKCSPG 60
QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVDDGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCIVDDGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTSPNGTLEECQ 180
QY 181 HQTCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
DB 181 HQTCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
QY 241 VQKROBAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
DB 241 VQKROBAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

RESULT 5

US-10-066-209-2
;; Sequence 2, Application US/10066209
;; Publication No. US20020115110A1
;; GENERAL INFORMATION:
;; APPLICANT: Brigham-Burke, Michael R.
;; APPLICANT: Young, Peter R.
;; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
;; FILE REFERENCE: GH-50030-D1
;; CURRENT APPLICATION NUMBER: US/10/066, 209
;; PRIOR FILING DATE: 2001-10-25
;; PRIOR APPLICATION NUMBER: 09/072, 993
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/055, 513
;; PRIOR FILING DATE: 1997-08-13
;; PRIOR APPLICATION NUMBER: 60/056, 980
;; PRIOR FILING DATE: 1997-08-26
;; PRIOR APPLICATION NUMBER: 60/057, 550
;; PRIOR FILING DATE: 1997-08-29
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 283
;; TYPE: PRT
;; ORGANISM: HOMO SAPIENS
US-10-066-209-2

Query Match 99.6%; Score 1572; DB 14; Length 283;
Best Local Similarity 99.6%; Pred. No. 2.5e-125;
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMSTPRTDVLRLVLYLTFIAGPCYAPALPSCKEDEYVSGCCPKCSPG 60
DB 1 MEPPGDMGPPPMSTPRTDVLRLVLYLTFIAGPCYAPALPSCKEDEYVSGCCPKCSPG 60
QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120

QY 121 CSPGHFCIVDDGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCIVDDGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTSPNGTLEECQ 180
QY 181 HQTCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
DB 181 HQTCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
QY 241 VQKROBAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
DB 241 VQKROBAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

RESULT 6

US-09-934-289A-42
;; Sequence 42, Application US/09934289A
;; Patent No. US20020132297A1
;; GENERAL INFORMATION:
;; APPLICANT: Busfield, Samantha J.
;; TITLE OF INVENTION: NOVEL MOLECULES OF THE
;; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
;; FILE REFERENCE: MB1098-061CPCIN (M)
;; CURRENT APPLICATION NUMBER: US/09/934, 289A
;; PRIOR FILING DATE: 2001-08-21
;; PRIOR APPLICATION NUMBER: US 09/342, 767
;; PRIOR FILING DATE: 1999-06-29
;; PRIOR APPLICATION NUMBER: US 09/146, 950
;; PRIOR FILING DATE: 1998-09-03
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 42
;; LENGTH: 277
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: (1)... (38)
US-09-934-289A-42

Query Match 87.0%; Score 1373.5; DB 10; Length 277;
Best Local Similarity 93.5%; Pred. No. 1.6e-108;
Matches 245; Conservative 2; Mismatches 6; Indels 9; Gaps 1;

QY 1 MEPPGDMGPPPMSTPRTDVLRLVLYLTFIAGPCYAPALPSCKEDEYVSGCCPKCSPG 60
DB 1 MEPPGDMGPPPMSTPRTDVLRLVLYLTFIAGPCYAPALPSCKEDEYVSGCCPKCSPG 60
QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCCDPMAGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVDDGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCIVDDGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTSPNGTLEECQ 180
QY 181 HQTCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
DB 181 HQTCSMLVTYKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKKRKRPGDVVKYIVS 240
QY 241 VQKROBAEGEATVIEALQAPP 262
DB 241 VQ-----VILILPLSLPP 253

RESULT 7

US-09-934-289A-44
;; Sequence 44, Application US/09934289A
;; Patent No. US20020132297A1
;; GENERAL INFORMATION:
;; APPLICANT: Busfield, Samantha J.
;; TITLE OF INVENTION: NOVEL MOLECULES OF THE

SEQ ID NO 18
LENGTH: 197
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-18

Query Match 67.2%; Score 1060; DB 10; Length 197;
Best Local Similarity 98.4%; Pred. No. 3.9e-82;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MPPGDWGPMPWRSTPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVSGECCPKCSPG 60
DB 1 MPPGDWGPMPWRSTPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVSGECCPKCSPG 60
QY 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLCQCCQCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLCQCCQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVOKGTESDTLCCNCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVOKGTESDTLCCNCPGTFSPNGTLEECQ 180
QY 181 HQTKCSW 187
DB 181 HQT--NW 185

RESULT 11
US-09-934-289A-30
Sequence 30, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: MB1098-061CPC1N1 (M)
CURRENT APPLICATION NUMBER: US/09/934, 289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 186
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-934-289A-30

Query Match 67.0%; Score 1058; DB 10; Length 186;
Best Local Similarity 99.5%; Pred. No. 5.5e-82;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPGDWGPMPWRSTPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVSGECCPKCSPG 60
DB 1 MPPGDWGPMPWRSTPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVSGECCPKCSPG 60
QY 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLCQCCQCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLCQCCQCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVOKGTESDTLCCNCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVOKGTESDTLCCNCPGTFSPNGTLEECQ 180

QY 181 HQTK 184
DB 181 HQTK 184

RESULT 12
US-09-934-289A-4
Sequence 4, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: MB1098-061CPC1N1 (M)
CURRENT APPLICATION NUMBER: US/09/934, 289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 155
TYPE: PRT
ORGANISM: Homo sapiens
US-09-934-289A-4

Query Match 53.7%; Score 847; DB 10; Length 155;
Best Local Similarity 98.0%; Pred. No. 3.3e-64;
Matches 146; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 39 LPSCKEDEYVSGECCPKCSPGYRVKACGELTGTVCPCPGTYIAHLNGLSKLCQCCQ 98
DB 1 LPSCKEDEYVSGECCPKCSPGYRVKACGELTGTVCPCPGTYIAHLNGLSKLCQCCQ 98
QY 99 CDPAMGLRASRNCSTENAVCGSPGHFCTVODGDHCAACRAVATSSPGQVOKGTESDTL 158
DB 61 CDPAMGLRASRNCSTENAVCGSPGHFCTVODGDHCAACRAVATSSPGQVOKGTESDTL 120
QY 159 DTLCQNCPPGTFSPNGTLEECQHQTCSW 187
DB 121 DTLCQNCPPGTFSPNGTLEECQHQTCSW 149

RESULT 13
US-09-934-289A-32
Sequence 32, Application US/09934289A
Patent No. US20020132297A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: MB1098-061CPC1N1 (M)
CURRENT APPLICATION NUMBER: US/09/934, 289A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/342,767
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/146,950
PRIOR FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 148
TYPE: PRT
ORGANISM: Homo sapiens
US-09-934-289A-32

Query Match 53.4%; Score 843; DB 10; Length 148;
Best Local Similarity 100.0%; Pred. No. 6.9e-64;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Camelox virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=203174;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DUBAI-1992 / CP-5, and SOMALIA-1978;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87840; AAB94357.1; -
DR EMBL; U87837; AAB94354.1; -
DR HSSP; Q92956; IJMA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 349 AA; 38036 MW; EA412AE8E6E09B4 CRC64;

Query Match 16.8%; Score 266.5; DB 12; Length 349;
Best Local Similarity 33.1%; Pred. No. 2.1e-18;
Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

QY 21 LRLVLTFLGAPC-----YAPALPSCKEDEVPGSECCPCSPGYRVKACGEL 70
DB 1 MSKLVSYILFLSCIIINGRDVTPVAPSGKCKDNEYRKHNLCLCSPGTYASRLCDSK 60
QY 71 TGTVEPCPPGTYIAHLNGLSKLQCO-MCDPAMGLRASRNCSTENAVCGSPGHFCTV 129
DB 61 TMTQCTPCSGDTFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCTL 118
QY 130 QGDGHCACRAVATSSPGORVQKGTESODTLQCNCPPTGSPN-CTLECOHOT 183
DB 119 KSSSGCRCTISKTKGIGYV-SGYTSTDVLCSPGPGTYSHYSTDKCEPVT 172

RESULT 14
057103
ID 057103 PRELIMINARY; PRT; 348 AA.
AC 057103;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Zaire-1979;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87847; AAB94364.1; -
DR HSSP; Q92956; IJMA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;

Query Match 16.8%; Score 265.5; DB 12; Length 348;
Best Local Similarity 32.0%; Pred. No. 2.6e-18;
Matches 56; Conservative 25; Mismatches 79; Indels 15; Gaps 5;

QY 21 LRLVLTFLGAPC-----YAPALPSCKEDEVPGSECCPCSPGYRVKACGEL 70

DB 1 MSKLVSYILFLSCIIINGRDVTPVAPSGKCKDNEYRKHNLCLCSPGTYASRLCDSK 60
QY 71 TGTVEPCPPGTYIAHLNGLSKLQCO-MCDPAMGLRASRNCSTENAVCGSPGHFCTV 129
DB 61 TMTQCTPCSGDTFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCTL 118
QY 130 QGDGHCACRAVATSSPGORVQKGTESODTLQCNCPPTGSPN-CTLECOHOT 183
DB 119 KSSSGCRCTISKTKGIGYV-SGYTSTDVLCSPGPGTYSHYSTDKCEPVT 172

RESULT 15
057099
ID 057099 PRELIMINARY; PRT; 349 AA.
AC 057099;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sierra Leone-1970;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87843; AAB94360.1; -
DR HSSP; Q92956; IJMA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 38321 MW; FE449028CC933F57 CRC64;

Query Match 16.8%; Score 265.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 2.6e-18;
Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

QY 21 LRLVLTFLGAPC-----YAPALPSCKEDEVPGSECCPCSPGYRVKACGEL 70
DB 1 MSKLVSYILFLSCIIINGRDVTPVAPSGKCKDNEYRKHNLCLCSPGTYASRLCDSK 60
QY 71 TGTVEPCPPGTYIAHLNGLSKLQCO-MCDPAMGLRASRNCSTENAVCGSPGHFCTV 129
DB 61 TMTQCTPCSGDTFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYYCTL 118
QY 130 QGDGHCACRAVATSSPGORVQKGTESODTLQCNCPPTGSPN-CTLECOHOT 183
DB 119 KALCCRTCTISKTKGIGYV-SGYTSTDVLCSPGPGTYSHYSTDKCEPVT 172
QY 190 T 190
DB 173 T 173

Search completed: November 14, 2003, 17:31:45
Job time : 43 secs

```

OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Benin-1978;
RA Loparev V.N., Parsons J.M., Eposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species.";
RL Submitted (JAN-1977) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87846; AAB94363.1; -.
DR HSSP; Q92956; IJMA.
DR InterPro; IPR01168; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SMO0208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 38308 MW; CBE2C949F9994C59C CRC64;

```

Query Match	17.1%;	Score 269.5;	DB 12;	Length 349;
Best Local Similarity	32.6%;	Pred. No. 1e-18;		
Matches 59;	Conservative 22;	Mismatches 81;	Indels 19;	Gaps 5;

[illegible]

RESULT	11	
057291		
AC	057291	PRELIMINARY;
ID	057291	PRT; 349 AA.
DT	01-JUN-1998	(TEMBLrel. 06, Created)
DT	01-JUN-1998	(TEMBLrel. 06, Last sequence update)
DT	01-MAR-2003	(TEMBLrel. 23, Last annotation update)
DE	Tumor necrosis factor receptor II homolog.	
DN	CRMB.	

0C Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
0C Orthopoxvirus.
0X NCBI_TaxID=10244;
0X

RN
 LI
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases

DR	EMBL; U087842; AAB943359.1; -
DR	EMBL; U087994; AAB943365.1; -
DR	EMBL; U087995; AAB943366.1; -
DR	EMBL; U080143; AAB943368.1; -
DR	HSSP; Q92956; LJMA.

```
DR PFam; PFO0020; TNFR_C6; 2_
DR SMART; SMO0208; TNFR; 2_
DR PROSITE; PS00682; TNFR_NGFR_1; 2
DR PROSITE; PS00500; TNFR_NGFR_2; 2
SQ SEQUENCE      349 AA;    38295 MW;    C
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Query Match	17.1%;	Score 269.5;	DB 12;	Length 349;
Best Local Similarity	32.6%;	Pred. No. 1e-18;		

	Matches	59; Conservative	22; Mismatches	81; Indels	19; Gaps	5;
QY	21	LRVLVYLFLCACP-----YAPRLPBCCKDEYFVPSGCCPKSPGIRVAVACCEL	70			
Db	1	MRSLVYSYILFLSCIINGRDIAHPABNGCKNEYRSRLCCLCLCPPTGYASRLCDCK	60			
QY	71	TGTVCEPCPEGTIVIAHLNGLSKCLQCC-MCDPAMGLASRNCSRRTENAVCGSPGHFCTV	129			
Db	61	TNTQCTPCGSDTPTFSHHNNHLQACLSGNCGRCC-SNQVETRSCNTHNRIGCSGYYCLL	118			
QY	130	QDGHCAACRAVYATSSPGQAVQKGTBSODTLCONCPPTGFSFNGTLEECOHQTKSMVLV	189			
Db	119	KGASGCRCTLSKTRCKGIGYGV-SGYTSTGDVICSPPCGGTYS-----HTVASDTPCKEPPV	172			
QY	190	T 190				
Db	173	T 173				

RESULT 12	
057098	
ID 057098	PRELIMINARY; PRT: 349 AA.

DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Camel痘x virus (strain CR-1).
OC Viruses; dsDNA viruses, no RNA stage; Chordopoxvirinae
OC Orthopoxvirus.
OX NCBI_TaxId=203174;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Saudi-M3.
RA Loparev V.N., Parsons J.M., Espósito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species";
RL Submitted (JUN-1997) to the EMBL/GenBank/DDA databases.

```
DR HSSP: Q92956; 1JMA.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SMO0208; TNFR; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 37978 MW; 8630EFAED7A584B5 CRC64;
```

Query Match	16.9%	Score	266.5	DB	12	Length	349
Best Local Similarity	33.1%	Prod	2.1e-18				
Matches	57	Conservative	24	Mismatches	76	Indels	15
						Gaps	5

QY LRLVLTPLTGLGAP-----TAPALPCKREDEYVVSSECCPKSPGGRVNEAAGEL 70
Dy 2 LRLVLTPLTGLGAP-----TAPALPCKREDEYVVSSECCPKSPGGRVNEAAGEL 70
Dy 1 MKSLVLSYLLFLSCIIINGRDVTPAPANGCKCKNEYRNHLCCLSLCPPTGVSRLDSK 60
Qy 71 TGVCPECPPEPTGYIAHLNGLSKLCIQQ--MCPAMGLASRNCRSTENAAGCSPGHCIV 129
Dy 61 TNYQCTPCSGGTFITSNHNLPACLSCNCRCD--SNQVETRSCNTHHRICECSPGYCIL 118
Qy 130 QQDQDCACAGATATSPGQRVQVKGGTSEQDPLLCNQCPPTGFSN-GLUEEQ 180
Dy 119 KSSGGKACVLSQTKGIGYV-SGHTASGADVICSPLGATYSKRVSSADCKE 169

RESULT 13	
057284	
ID 057284	PRELIMINARY;
AC 057284;	PRT; 349 AA

DT	01-JUN-1998	(TREMBLrel. 06, last sequence update)
DT	01-MAR-2003	(TREMBLrel. 23, last annotation update)

KW Receptor.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;
Query Match 17.1%; Score 269.5; DB 12; Length 348;
Best Local Similarity 32.6%; Pred. No. 1e-18;
Matches 57; Conservative 25; Mismatches 78; Indels 15; Gaps 5;
QY 21 LRLVLYLTLFLGAPC-----YAPALPSCKEDEVPGSECCPKCSGYRYKACGEL 70
DB 1 MRSVLVSYLLFLSCIIINGRDIAHPAPNSGKCKDNEYRSRLCLSCPPGTAYASRLCDSK 60
QY 71 TGTVCPCPPGTGYIAHLNGLSKLCCQ-MCDPAMGLRASRNCRTENAVCGSPGHFCTV 129
DB 61 TTTQCTPCGSDTFTSHNNHLQCLSCNGRCD--SNQVETRSCNTTNRICCEGSPGYICLL 118
QY 130 QDGDHCACRAVATSSPGQRYVQKGTESODTLCCNCPGTFSFN-GTLEECQHQT 183
DB 119 KSSGCRCTISKTKGIGYGV-SGYTSTGDVLCSPCGPETYSHVSTDKCEPVT 172

RESULT 8

OS71277 PRELIMINARY; PRT; 348 AA.
AC 057101
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog (J2L).
GN CRMB OR J2R OR J2L.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN 11
RN SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1996 / 96-17, and ZAIRE-1996 / 96-16;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN 12
RN SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-96-I-16;
RA MEDLINE=21592287; PubMed=11734207;
RA Ryazankina O.I., Tolmenin A.V., Babkin I.V., Saitonov P.F.,
RA Shchelnikov S.N., Tolmenin A.V., Gutorov V.V., Uvarova E.A.,
RA Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,
RA Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss B.,
RA Sandakchiev L.S.;
RT "Human monkeypox and smallpox viruses: genomic comparison.";
RL FEBS Lett. 509:66-70(2001).
RN 13
RN SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-96-I-16;
RA Shchelnikov S.N., Tolmenin A.V., Saitonov P.F., Gutorov V.V.,
RA Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,
RA Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakchiev L.S.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL; U87841; AAB94358.1; -
DB EMBL; U87841; AAB94358.1; -
DB EMBL; AF380138; AAL40648.1; -
DB HSSP; Q92956; JMA.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;

Query Match 17.1%; Score 269.5; DB 12; Length 348;
Best Local Similarity 32.6%; Pred. No. 1e-18;
Matches 57; Conservative 25; Mismatches 78; Indels 15; Gaps 5;
QY 21 LRLVLYLTLFLGAPC-----YAPALPSCKEDEVPGSECCPKCSGYRYKACGEL 70
DB 1 MRSVLVSYLLFLSCIIINGRDIAHPAPNSGKCKDNEYRSRLCLSCPPGTAYASRLCDSK 60
QY 71 TGTVCPCPPGTGYIAHLNGLSKLCCQ-MCDPAMGLRASRNCRTENAVCGSPGHFCTV 129
DB 61 TTTQCTPCGSDTFTSHNNHLQCLSCNGRCD--SNQVETRSCNTTNRICCEGSPGYICLL 118
QY 130 QDGDHCACRAVATSSPGQRYVQKGTESODTLCCNCPGTFSFN-GTLEECQHQT 183
DB 119 KSSGCRCTISKTKGIGYGV-SGYTSTGDVLCSPCGPETYSHVSTDKCEPVT 172

DB 1 MRSVLVSYLLFLSCIIINGRDIAHPAPNSGKCKDNEYRSRLCLSCPPGTAYASRLCDSK 60
QY 71 TGTVCPCPPGTGYIAHLNGLSKLCCQ-MCDPAMGLRASRNCRTENAVCGSPGHFCTV 129
DB 61 TTTQCTPCGSDTFTSHNNHLQCLSCNGRCD--SNQVETRSCNTTNRICCEGSPGYICLL 118
QY 130 QDGDHCACRAVATSSPGQRYVQKGTESODTLCCNCPGTFSFN-GTLEECQHQT 183
DB 119 KSSGCRCTISKTKGIGYGV-SGYTSTGDVLCSPCGPETYSHVSTDKCEPVT 172

RESULT 9

OS7101 PRELIMINARY; PRT; 349 AA.
AC 057101
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN 11
RN SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1977;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DB EMBL; U87845; AAB94362.1; -
DR HSSP; Q92956; JMA.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 38311 MW; 02F65B00C8B58BE CRC64;

Query Match 17.1%; Score 269.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 1e-18;
Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

QY 21 LRLVLYLTLFLGAPC-----YAPALPSCKEDEVPGSECCPKCSGYRYKACGEL 70
DB 1 MRSVLVSYLLFLSCIIINGRDIAHPAPNSGKCKDNEYRSRLCLSCPPGTAYASRLCDSK 60
QY 71 TGTVCPCPPGTGYIAHLNGLSKLCCQ-MCDPAMGLRASRNCRTENAVCGSPGHFCTV 129
DB 61 TTTQCTPCGSDTFTSHNNHLQCLSCNGRCD--SNQVETRSCNTTNRICCEGSPGYICLL 118
QY 130 QDGDHCACRAVATSSPGQRYVQKGTESODTLCCNCPGTFSFN-GTLEECQHQT 189
DB 119 KSSGCRCTISKTKGIGYGV-SGYTSTGDVLCSPCGPETYSHVSTDKCEPVT 172
QY 190 T 190
DB 173 T 173
RESULT 10
OS7102 PRELIMINARY; PRT; 349 AA.
AC 057102
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

QY 141 YATSSPGORVOKGTESDTLQONCPGTF5-PNGTLEBEOHQTKC-SMLVTKAGAGTSS 198
 Db 122 HSLCPGAGVOKMATEVSDTICEPCVPGFSSVSSASKECQPMWTSCKSKGLVEQAAGNK 181
 QY 199 SHWVWFSSGLVIVVSTVGLICVKKRKRGRGVKVIYSVQKRDPAEAGEA----- 252
 Db 182 TDVCGFGFSRRKALVIRITIGILPA-----VLLVFLCIRKVTKEOTKALHPKTE 232
 QY 253 --TVIEA--LQAPDVTVAVEETI 273
 Db 233 RQDPVETIDLEDFD-STAPVOETL 256

RESULT 5

Q8K2X6 PRELIMINARY: PRT; 289 AA.
 ID 08K2X6
 AC 08K2X6:
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Similar to tumor necrosis factor receptor superfamily, member 5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straubeberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029254; AAH29254.1; -
 DR InterPro; IPR001005; Myb DNA binding.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR_4.
 DR PROSITE; PS00037; MYB_1; 1.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.
 KM Receptor.
 SQ SEQUENCE 289 AA; 32077 MW; DBE93B1E439F1E2A CRC64;

Query Match 17.8%; Score 280.5; DB 11; Length 289;
 Best Local Similarity 27.9%; Pred. No. 6.6e-20;
 Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;

QY 41 SCKEDEYFVSGECCPKSPGYRVKACGELTGVCEPCPGTYIAHLNGLSKLCQCMCD 100
 Db 25 TCSDKQYLDHQCCDLQPGSRSLTSHCTALEKTCCHPEDSGEFAQWNRIRCHQHRC 84
 QY 101 PAMGLASRNCSRTENAVCGSPGHFCTVQGDHCACRAVATSSPGORVOKGTESDT 160
 Db 85 PNOGLRVKRGSTASDVTVCACKEGQHTSKD---CEACAQHTPCIPIFGVWEMATEETDT 141
 QY 161 LCQNCPPGTFSFNGTL-BECHOHTKCS---MLVTKAGAGTSSHWVWFSSGLVIV 215
 Db 142 VCHCPCVPGFSSVSSASKECQPMWTSCKSKGLVEQAAGNK 181
 QY 216 CSTVGLITC-----VNR--RKRPGDVVIVSVORKEAGEATVTEALQAPDVTT 266
 Db 199 PVWVGILITIFGVFLYIKVKKPKDN--ELPPAARQDPQEME-----DYFGNTA 249
 QY 267 VAVEETI 273
 Db 250 APVOETL 256

RESULT 6

057100 PRELIMINARY: PRT; 349 AA.
 AC 057100;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Tumor necrosis factor receptor II homolog.
 OS CRMB.
 OS Morkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Nigeria-1971;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT "DNA sequence analysis as a criterion for allocation of the
 RT orthopoxviruses to a particular species."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U87844; AAB94361.1; -
 DR HSSP; Q92956; JUMA.
 DR InterPro; IPR001368; TNFR_c6.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR_2.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 KM Receptor.
 SQ SEQUENCE 349 AA; 38239 MW; DFC280D478F2422 CRC64;

Query Match 17.2%; Score 271.5; DB 12; Length 349;
 Best Local Similarity 32.6%; Pred. No. 6.6e-19;
 Matches 59; Conservative 23; Mismatches 80; Indels 19; Gaps 5;

QY 21 LRVLVYTLFLGAPC-----YAPALPSCKEDEYFVSGECCPKSPGYRVKACGEL 70
 Db 1 MRSVLYSYILFLSCIINGRDIAHPASNGCKDNEYRSNNLCLSCPPTVASRLCDSK 60
 QY 71 TGYVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLASRNCSRTENAVCGSPGHFCTIV 129
 Db 61 TNYQCTPGSGDFTSHNNHQAQCLSCNGRCD--SNQVETSCVTHNRIRCECSPGYVCL 118
 QY 130 QDDGHCACRAVATSSPGORVOKGTESDTLQONCPGTFSPNGTLEBEOHQTKCSMLV 169
 Db 119 KASGCGSTCIKTKGIGIV-SGYTSTGDVICSPOCGFY----HTVSTDKCPVV 172
 QY 190 T 190
 Db 173 T 173

RESULT 7

057108 PRELIMINARY: PRT; 348 AA.
 ID 057108
 AC 057108;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Tumor necrosis factor receptor II homolog.
 OS CRMB.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Zaire-1970;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT "DNA sequence analysis as a criterion for allocation of the
 RT orthopoxviruses to a particular species."
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88142; AAB94367.1; -
 DR HSSP; Q92956; JUMA.
 DR InterPro; IPR001368; TNFR_c6.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR_2.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.

QY 61 YRVKACGELTGVCPCPCPGTCTIATLNGLSKLCLOCOMCDPAMGLASRNCSTENAVCG 120
 DB 61 FHVRAQAGTQTCVPCPCPGTCTIATLNGLSKLCLOCOMCDPAMGLASRNCSTENAVCG 120
 QY 121 CSPGHCITVODGDHCAACRAVATSSPGORVOKGTSODTLCNCPGTFSPNGTLEECQ 180
 DB 121 CSPGHCITVODGDHCAACRAVATSSPGORVOKGTSODTLCNCPGTFSPNGTLEECQ 180
 QY 181 HQTKCS-WLVTKAGACTSSSHWWMFLSGSLVIVICSTV--GLIICVRRKRGDVVY 237
 DB 181 HGKCKCKMLVTEAGPCTSSSRWMMFLSGSLVIVIGLIIILIIICVRRKRGDVVY 240
 QY 238 IYSVORROABEGEATVIALQAPDVTTVAVEETIPSTGTS 280
 DB 241 IYSVORROABEGEATVTEAVQAPDITTVAVETEPALFGTS 283

RESULT 2

Q8N634 PRELIMINARY; PRT; 199 AA.
 AC Q8N634;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Similar to tumor necrosis factor receptor superfamily, member 14 (hepervirus entry mediator).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC029848; AAH29848.1; -
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 1.
 KW Receptor.
 SQ SEQUENCE 199 AA; 21404 MW; F04A2264BC16D00A CRC64;

Query Match 62.0%; Score 978; DB 6; Length 199;
 Best Local Similarity 99.5%; Pred. No. 3.9e-90;
 Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 PAMGLASRNCSTENAVCGSPGHCITVODGDHCAACRAVATSSPGORVOKGTSODT 160
 DB 17 PAMGLASRNCSTENAVCGSPGHCITVODGDHCAACRAVATSSPGORVOKGTSODT 76
 QY 161 LCNCPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSSHWWMFLSGSLVIVICSTVG 220
 DB 77 LCNCPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSSHWWMFLSGSLVIVICSTVG 136
 QY 221 LIICVRRKRGDVVYVIVSVORROABEGEATVIALQAPDVTTVAVEETIPSTGTS 280
 DB 137 LIICVRRKRGDVVYVIVSVORROABEGEATVIALQAPDVTTVAVEETIPSTGTS 196
 QY 281 PNH 283
 DB 197 PNH 199

RESULT 3

Q8VC17 PRELIMINARY; PRT; 196 AA.
 AC Q8VC17;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Hypothetical 21.6 kDa protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC022125; AAH22125.1; -
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS0050; TNFR_NGFR_2; 1.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 196 AA; 21555 MW; 2AB3FF8905E260E8 CRC64;

Query Match 24.4%; Score 384.5; DB 11; Length 196;
 Best Local Similarity 42.4%; Pred. No. 1.5e-30;
 Matches 84; Conservative 24; Mismatches 73; Indels 17; Gaps 4;

QY 82 TYIAHNGLSKLCLOCOMCDPAMGLASRNCSTENAVCGSPGHCITVODGDHCAACRAV 141
 DB 2 TYIAHNGLSKLCPCGVCDDPWGLTTWQCSWKDVCRCITGFCENQDGHSCSTCLOH 61
 QY 142 ATSSPGORVOKGTSODTLCNCPGTFSPNGTLEECQHQTKCSWLVTKAGAGTS----- 197
 DB 62 TTCPCGQVKKRGTHDQDVICADCLGTFTSLGCTDECLPWNCSAFQGVVRRGNTSTOT 121
 QY 198 --SSHWWMFLSGSLVIVIV-CSTVGLIICVRRKRGDVVYVSVORROABEGEATV 254
 DB 122 TCSQVYVYVSIILPLVIVGVIGIAGFLICTRRHHTSSVAKELEPFQEOOE----- 174
 QY 255 IEALQAPDVTTVAVEET 272
 DB 175 -NTIRFP--VTEVGPAET 189

RESULT 4

Q8SQ34 PRELIMINARY; PRT; 278 AA.
 AC Q8SQ34;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE CD40.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxId=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA West K.A., Li A.W., Rowden G.;
 RT "Characterization of the Porcine CD40 Molecule."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF248545; AAL92924.1; -
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 4.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS0050; TNFR_NGFR_2; 4.
 SQ SEQUENCE 278 AA; 30951 MW; 20D446B4AF93DD2 CRC64;

Query Match 21.0%; Score 332; DB 6; Length 278;
 Best Local Similarity 31.7%; Pred. No. 4.2e-25;
 Matches 84; Conservative 46; Mismatches 109; Indels 26; Gaps 8;

QY 21 LRLVLYLTFGLAPCAPALPSCKEDEYPVGSCPCPCSPGVKACGELTGVCPCPP 80
 DB 6 LKCLMGLCFLTVVHEPP-TSCKENQYPTNSCCNLCPGQGLVNHCTVETTECLPSS 64
 QY 81 GTYIAHNGLSKLCLOCOMCDPAMGLASRNCSTENAVCGSPGHCITVODGDHCAACRA 140
 DB 65 SEFLATWNRKCHQHKYCDPMLGLQVQREGTSKIDTTVCVSGEHHHC--TNSACSSCTL 121

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:28:10 ; Search time 41 Seconds
(without alignments)
1781.192 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578
Sequence: 1 MEPPGDMGPPMWRSTPRTDV.....VTVAVERTIPSTGSRPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: SPTREMBL_23:*
 - 2: sp_archaea:*
 - 3: sp_bacteria:*
 - 4: sp_fungi:*
 - 5: sp_human:*
 - 6: sp_invertebrate:*
 - 7: sp_mhc:*
 - 8: sp_mammal:*
 - 9: sp_organelle:*
 - 10: sp_phage:*
 - 11: sp_plant:*
 - 12: sp_prodent:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1303.5	82.6	283	6	Q9XSZ8
2	978	62.0	199	4	Q8N634
3	384.5	21.4	196	11	Q8VC17
4	332	21.0	278	6	Q8SQ34
5	280.5	17.8	289	11	Q8K2X6
6	271.5	17.2	349	12	Q57100
7	269.5	17.1	348	12	Q57108
8	269.5	17.1	348	12	Q57277
9	269.5	17.1	349	12	Q57101
10	269.5	17.1	349	12	Q57102
11	269.5	17.1	349	12	Q57291
12	266.5	16.9	349	12	Q57284
13	266.5	16.9	349	12	Q57284
14	265.5	16.8	349	12	Q57103
15	265.5	16.8	349	12	Q57099
16	262.5	16.6	349	12	Q57097

17	262	16.6	169	11	Q9JKE0	Q9JKE0	rattus norv
18	259	16.4	349	12	Q57111	Q57111	variola vir
19	257.5	16.3	348	12	Q57112	Q57112	variola vir
20	257.5	16.3	351	12	Q57117	Q57117	compos viru
21	257	16.3	277	6	Q8WMO2	Q8WMO2	ovis aries
22	257	16.3	349	12	Q57110	Q57110	variola vir
23	254.5	16.1	438	13	Q9DFV0	Q9DFV0	brachydanio
24	249	15.8	349	12	Q57109	Q57109	variola vir
25	239	15.1	350	12	Q57116	Q57116	compos viru
26	236.5	15.0	351	12	Q57121	Q57121	compos viru
27	232.5	14.7	349	12	Q57305	Q57305	compos viru
28	229.5	14.5	326	12	Q57122	Q57122	compos viru
29	229	14.5	347	12	Q57119	Q57119	compos viru
30	228.5	14.5	326	12	Q57120	Q57120	compos viru
31	228	14.4	312	13	Q9DGH8	Q9DGH8	gallus gall
32	228	14.4	360	12	Q57118	Q57118	compos viru
33	227	14.4	285	13	Q9DGH7	Q9DGH7	gallus gall
34	226.5	14.4	350	12	Q57123	Q57123	compos viru
35	225.5	14.3	347	12	Q57115	Q57115	compos viru
36	225.5	14.3	355	12	Q85308	Q85308	compos viru
37	219.5	13.9	267	6	Q02764	Q02764	oryctolagus
38	219.5	13.9	319	6	Q9TV79	Q9TV79	oryctolagus
39	218	13.8	320	6	Q9XS29	Q9XS29	oryctolagus
40	218	13.8	433	11	Q912M6	Q912M6	rattus norv
41	216	13.7	328	6	Q9BDP0	Q9BDP0	alotus trivi
42	215.5	13.7	263	6	Q9XS60	Q9XS60	oryctolagus
43	214.5	13.6	457	4	Q8IVS6	Q8IVS6	homo sapien
44	213.5	13.5	320	12	Q57079	Q57079	compos viru
45	213.5	13.5	417	11	Q8BY11	Q8BY11	mus musculu

ALIGNMENTS

RESULT 1

Q9XSZ8 ID Q9XSZ8 PRELIMINARY; PRT; 283 AA.

AC Q9XSZ8; 01-NOV-1999 (TREMURel. 12, Created)

DT 01-NOV-1999 (TREMURel. 12, Last sequence update)

DT 01-MAR-2003 (TREMURel. 23, Last annotation update)

DE HVEAS.

GN HVEAS.

OS Cercopithecus aethiops (Green monkey) (Grivet).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheidae; Cercopithecus.

OX NCBI_TaxID=9534;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=99256730; PubMed=1036573;

RA Foster T.P., Choulienko V.N., Kousoulas K.G.;

RT "Functional characterization of the HVEA homolog specified by African green monkey kidney cells with a herpes simplex virus expressing the green fluorescence protein.";

RL Virology 258:365-374(1999).

DR EMBL: AF147720; AAD37381.1; -.

DR HSBP; Q92956; JUMA.

DR InterPro: IPR001368; TNFR_c6.

DR Pfam: PF00020; TNFR_c6; 3.

DR SMART: SM00208; TNFR_3.

DR PROSITE: PS00652; TNFR_NGFR_1; 1.

DR PROSITE: PS50050; TNFR_NGFR_2; 2.

SQ SEQUENCE 283 AA; 397951C6617FE3AA CRC64;

Query Match 82.6%; Score 1303.5; DB 6; Length 283;

Best Local Similarity 82.0%; Pred. No. 1.2e-122;

Matches 232; Conservative 18; Mismatches 30; Indels 3; Gaps 2;

QY 1 MEPPGDMGPPMWRSTPRTDVLRVLVLTFLGACVAPALPSCKEDEYVSGCCPKGPG 60

1 MEPPGDMGPPMWRSTPRTDVLRVLVLTFLGACVAPALPSCKEDEYVSGCCPKGPG 60

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SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;
 Query Match 15.2%; Score 240.5; DB 1; Length 271;
 Best Local Similarity 34.9%; Pred. No. 2.8e-12;
 Matches 51; Conservative 16; Mismatches 54; Indels 25; Gaps 5;

QY 41 SCKEDYPIVGSSECCPFCSPGKRYKAEAGELTGVCEPCPGTITAHNLGSLKCLQCOMD 100
 DB 25 NCVKOTYPSGHHKCRRCQPHGMVSRCDHTDRTVCHCEPGFYNEAVN-YDTCKQCTQCN 83
 QY 101 PMWGLASRNCSTRTEAVCGSPGHFCIVQDGDHCAACRAVATSPGKRVOKGTESDPT 160
 DB 84 HNSGSLKQNCCTEDTETVQCCRRG-TQPRDSSH-----KLGVN----- 121
 QY 161 LCQNCPPGTFSPNGTLEBEOHOTKCS 186
 DB 122 -CVPCPPGHFSP-GSNQACKFMTNCT 145

RESULT 14
 ID_VT2_MYXVL STANDARD; PRT; 326 AA.
 AC P29825;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor soluble receptor precursor (Protein T2).
 GN M002L OR T2.
 OS Myxoma virus (strain Lausanne).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Leporipoxvirus.
 NC NCB1_TaxID=31530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91335768; PubMed=1651597;
 RA Upton C., Macen J.L., Schreiber M., McFadden G.;
 RT "Myxoma virus encodes a secreted protein with homology to the tumor
 necrosis factor receptor gene family that contributes to viral
 virulence."
 RL Virology 184:370-382(1991).
 RP [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20032073; PubMed=10562494;
 RA Cameron C., Hora-Witchell S., Chen L., Barrett J., Cao J.X.,
 RA Macalalay C., Miller D., Evans D., McFadden G.;
 RT "The complete DNA sequence of myxoma virus."
 RL Virology 264:298-318(1999).
 CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
 ANTIVIRAL EFFECTS OF THE CYTOKINE.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 CC -----
 DR EMBL: M95181; AAA46632.1; -;
 DR EMBL: AF170726; AAP15046.1; -;
 DR EMBL: AF170726; AAP14887.1; -;
 DR EMBL: A23729; CA01688.1; -;
 DR PIR: A40566; GQVZML.
 DR HSSP: P19438; INCF.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PR00020; TNFR_c6; 2.
 DR SMART: SM00208; TNFR_3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00652; TNFR_NGFR_2; 2.
 KM Receptor; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 326
 FT REPEAT 27 62
 FT REPEAT 63 104
 FT REPEAT 105 147
 FT REPEAT 148 186
 FT DISULFID 28 39
 FT DISULFID 40 53
 FT DISULFID 43 61
 FT DISULFID 64 79
 FT DISULFID 82 96
 FT DISULFID 86 104
 FT DISULFID 106 120
 FT DISULFID 123 146
 FT DISULFID 129 149
 FT DISULFID 164 185
 FT CARBOHYD 66 66
 FT CARBOHYD 181 181
 FT CARBOHYD 205 205
 FT CARBOHYD 238 238
 SQ SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;

Query Match 15.1%; Score 238.5; DB 1; Length 326;
 Best Local Similarity 26.8%; Pred. No. 4.9e-12;
 Matches 73; Conservative 30; Mismatches 104; Indels 65; Gaps 11;

QY 20 VARLVLYLFL-----GAPCYAPALPSCKEDYPIVGSSECCPFCSPGKRYKAEAGELTGT 73
 DB 1 MRLTLTLAYVACVYGGAP-YGADRGRKRGNDYERDGLCTCSCPGYSASRLCGGSDT 59
 QY 74 VCEPCPGTYIHLNLGSLKCLQCO-MCDPAMGLASRNCSTRTEAVCGSPGHFCIVQDG 132
 DB 60 VCSPCNERTFTASTHAPACVSCRRGCT--TGLHLSQSQCDKTRDRVCDSSAGNYCLLKKQ 117
 QY 133 DHCAACRAVATSPGKRVOKGTESDPTLCQNCPPETSPN-GTLEECO----- 180
 DB 118 EECRLIC-APKTCAPAGYGVSGHTRGDVLCCTCPRTYSDAVSLETCTSSFNYSVEPN 176
 QY 181 ----HQTQSMVLVTAGA-----GTSSHHVWVWFLSGS 209
 DB 177 LYPVNDTCT--TTAGPNEVVKTSFVSYTLNHTDQDPVFTREYVIGTSBEGAGCFPTQM 233
 QY 210 ---LVIVICSTVGLICVKKRRKPRGDVVKV 238
 DB 234 DRYQNTTKMCTINIRCYE-----GDAVRTI 260

RESULT 15
 ID_TNFR6_PIG STANDARD; PRT; 332 AA.
 AC 077736;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
 DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
 DE (CD95).
 GN TNFRSF6 OR APT1 OR FAS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NC NCB1_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
 RT "Expression of apoptosis-associated genes in hibernating and stunned
 RT myocardium of pig."
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting deac-
 CC tivating signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC mediated apoptosis may have a role in the induction of peripheral

28-FEB-2003 (Rel. 41, Last annotation update)
 DE Soluble TNF receptor II precursor (cytokine response modifying protein
 B).
 GN (CRM1 OR D2L) AND (CRM2 OR H4R).
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GRI-90 / Grishak.
 RA MEDLINE=968229462; PubMed=9568042;
 RA Shchelkunov S.N., Saitonov P.F., Totmenin A.V., Petrov N.A.,
 RA Ryzankina O.I., Gutovov V.V., Kotwal G.J.;
 RA "The genomic sequence analysis of the left and right species-specific
 RA terminal region of a cowpox virus strain reveals unique sequences and
 RA a cluster of intact ORFs for immunomodulatory and host range
 RA proteins.";
 RT Virology 243:432-460(1998).
 RL [2]
 RN FUNCTION.
 RP STRAIN=Brighton red;
 RC MEDLINE=94378510; PubMed=8091665;
 RA Hu F.Q., Smith C.A., Pickup D.J.;
 RA "Cowpox virus contains two copies of an early gene encoding a soluble
 RT secreted form of the type II TNF receptor.";
 RL Virology 204:343-356(1994).
 CC -1- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
 CC the modification of TNF-mediated antiviral processes.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
 CC -----
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 CC -----
 DR EMBL: Y11842; CAA72578.1; -
 DR EMBL: Y15035; CAA75306.1; -
 DR HSSP: O14763; 1D0G.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 2.
 DR SMART: SM00208; TNFR_3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR Receptor; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 351 SOLUBLE TNF RECEPTOR II.
 FT REPEAT 31 67 TNFR-CYS 1.
 FT REPEAT 69 110 TNFR-CYS 2.
 FT DISULFID 32 43 BY SIMILARITY.
 FT DISULFID 44 57 BY SIMILARITY.
 FT DISULFID 47 67 BY SIMILARITY.
 FT DISULFID 70 85 BY SIMILARITY.
 FT DISULFID 88 102 BY SIMILARITY.
 FT DISULFID 92 110 BY SIMILARITY.
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 351 AA; 38253 MW; 57CAE73EF4E5D7C7 CRC64;
 Query Match 15.4%; Score 243.5; DB 1; Length 351;
 Best Local Similarity 31.0%; Pred. No. 2,1e-12;
 Matches 54; Conservative 27; Mismatches 76; Indels 17; Gaps 6;
 QY 21 LRLVLYLFLGLGAPC-----YAPALPSCKEDEYVSGECCKPKSPGRVVEAGCEL 70
 DB 1 KKSLVSYILFLSLCIINGRDIAHPASNGCKDNEYNRHNLCLSCPPGYASRLDSSK 60
 QY 71 --TGTVECPPTGYIAHLNGLSKLCCQ--MCDPAMGLASRNCSTRENNAVCGSPGHFC 127

61 TTNITQCTPGSGGFTSRNHLPAFLSCNGRCD--SNQVETRSCNTHNRICECAPGYGC 118
 QY 128 IVQGDHCACRAATATSSPGQVQKGTESDPTLCQCPPTSPFN-GTLEECQ 180
 DB 119 LKSGSGCKACVSTQKCGIGYV-SGHTSTGADVCSPCGIGTYSHTVSADKCE 171
 RESULT 13
 ID TNFR4_RAT STANDARD; PRT; 271 AA.
 AC P15725;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
 DE receptor) (OX40 antigen) (MRC OX40).
 GN TNFRSF4 OR TXGPIL OR OX40.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=90214614; PubMed=2157591;
 RA Mallett S., Fossum S., Barclay A.N.;
 RA "Characterization of the MRC OX40 antigen of activated CD4 positive T
 RT lymphocytes - a molecule related to nerve growth factor receptor.";
 RL EMO J. 9:1063-1068(1990).
 CC -1- FUNCTION: Receptor for TNFRSF4/OX40L/GP14.
 CC -1- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAFs (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 CC -----
 DR EMBL: X17037; CAA34897.1; -
 DR PIR: S12783; S12783.
 DR HSSP: O14763; 1D4V.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR SMART: SM00208; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 271 TUMOR NECROSIS FACTOR RECEPTOR
 FT DOMAIN 20 210 SUPERFAMILY MEMBER 4.
 FT DOMAIN 211 235 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 25 60 TNFR-CYS 1.
 FT REPEAT 61 102 TNFR-CYS 2.
 FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
 FT REPEAT 124 164 TNFR-CYS 4.
 FT DISULFID 26 37 BY SIMILARITY.
 FT DISULFID 38 51 BY SIMILARITY.
 FT DISULFID 41 59 BY SIMILARITY.
 FT DISULFID 62 76 BY SIMILARITY.
 FT DISULFID 79 94 BY SIMILARITY.
 FT DISULFID 82 102 BY SIMILARITY.
 FT DISULFID 104 122 BY SIMILARITY.
 FT DISULFID 125 138 BY SIMILARITY.
 FT DISULFID 144 163 BY SIMILARITY.
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143

Matches 69; Conservative 16; Mismatches 88; Indels 22; Gaps 8;

QY 16 PRDVLRLVLYLFLGAPCAPALPSCKE-DEYP-----VGSE-CCPKSPGKRYVEAGC 68
 DB 7 PGLSLCLVLYALPAL---LPFPAVRGVALEPTYPMDAETGERLVQAQCPGTFVGRPCR 63
 QY 69 ELTGTCVCEPCPGPTGYIAHLNGLSKCLQCCQMDPAMGLR--ASRNCSTENAVAGCSPGHF 126
 DB 64 RDSPTTCGPPPHNYQFMYLYLR---CRVCNVLGCEGEEEAACATINRACRGTGFF 120
 QY 127 CIVQDDHCAACRAVATSSPGRVQKGTESQDTLCQCPGTFPS-PNGTLEECQHQTQC 185
 DB 121 A-----HAGFCLEHASCPGAGVIAVGTSPQNTQCPGTFPSASSSSSEGCQPHRNC 174
 QY 186 SMVTYKAGAGTSSSH 200
 DB 175 TALGLALNVPGSSSH 189

RESULT 11
 ID TNR3_MOUSE STANDARD; PRT; 415 AA.
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (lymphotoxin-beta receptor).
 GN LTBR OR TNFRSF3 OR TNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RC MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RA "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression.";
 RT J. Immunol. 155:5280-5288 (1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96153885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RA "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping.";
 RT Genomics 30:312-319 (1995).
 RN (3)
 RP INTERACTION WITH TRAF5.
 RC STRAIN=BALB/C;
 RC MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbot L., Ware C.F.,
 RA Yagita H., Okumura K.;
 RA "TRAF5, an activator of NF-kappaB and putative signal transducer for
 RT the lymphotoxin-beta receptor.";
 RT J. Biol. Chem. 271:14661-14664 (1996).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and lTB. and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs
 CC (By similarity).
 CC -1- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.
 CC Associates with TRAF3 and TRAF4 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
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 CC or send an email to license@isb-sib.ch).

CC EMBL: U29173; AAA68964.1; -
 CC EMBL: L38423; AAB00846.1; -
 CC DR EMBL: U30798; AAB1334.1; -
 CC DR HSSP: O14763; 1D0G.
 CC DR MGD: MG1:104875; Ltbr.
 CC DR InterPro: IP001368; TNFR_c6.
 CC DR Pfam: PF00020; TNFR_c6; 3.
 CC DR SMART: SM00208; TNFR; 3.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 CC DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 CC KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 415
 FT FT
 FT DOMAIN 31 223
 FT TRANSMEM 224 244
 FT DOMAIN 245 415
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 170
 FT REPEAT 171 213
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 62 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 150
 FT DISULFID 142 169
 FT DISULFID 172 187
 FT CARBOHYD 40 40
 FT CARBOHYD 179 179
 FT SEQUENCE 415 AA; 44956 MW; 298326A56AEF61 CRC64;

Query Match 15.6%; Score 245.5; DB 1; Length 415;
 Best Local Similarity 25.9%; Pred. No. 1,7e-12;
 Matches 83; Conservative 40; Mismatches 115; Indels 83; Gaps 15;

QY 7 WGP-----PPMRSPRTDVLRLVLYLFLGAPCAPALPSCKEDEY-- 47
 DB 14 WEPULLIGSLGLVVASQPOLVPPRYENOT-----CMD-----QDKETYE 52
 QY 48 PVGSECCPKSPGKRYVEAGCGLGTVCPCPGTYIAHLNGLSKCLQCCQMDPAMGLR 107
 DB 53 PNHVCCSRCPGPFVFAVCSRSQDTVCCKTCHNSYNEHMHLSITCOLCRPCDYLGFEE 112
 QY 108 SRNCSTENAVAGCSPGHFCTIVQDD--HCAACRAVATSSPGRVQKGTESQ----- 158
 DB 113 VAPCTSDRAKRCRCOPGMSCVLDMECVACEERLV-----LCQPTAEAVTDEIMD 164
 QY 159 -DTLCQCPGTF-----SPNGTLEECQHQTQCSML-VTKAGAGTSSSHV----- 202
 DB 165 TDVNCVPCKPGHFOUNTSPRA---RCQPTREIGQLVLAAGTISDITCKNPPRGAM 221
 QY 203 -WFLSGSLVIVIVSTVGLICVKKRPRGDVVKVIVSVORROBAEGEATVTEALQAP 261
 DB 222 LLALILSLVLFLLFTTV--LACAWMRHP--SLCKRLGTLKRHPGE-ESPPCAPRAD 276
 QY 262 PDVTYVAVEETPSPFGSPN 282
 DB 277 PHEPDLA-BPLPLMSGDLSPS 296

RESULT 12
 ID CRMB_COMPX STANDARD; PRT; 351 AA.
 AC 073559;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

Db 117 TSKRTQRCOPGMECAAM-ALECHCELLSDCPGTEALKEDEVGKGNH-----CVPC 170
 QY 166 PPGTF-----SPNGTLEBEOHQTKC-SWLVTKAGACTSSSHWYWM-----FLSGSLVI 212
 Db 171 KAGHQNNTSSPSA-----RCQPHRCGNQGLVEAPAPTAQSDPTCKKPLEPLREPMGSTYLM 227
 QY 213 VIVCTVGLIIT-----CVKRRKRGDVVKYIVQRRQDAEAEATVIALQAP----- 261
 Db 228 LAVLLPLAFPLLATVFCSCIMWSPH--SLCRKLGLSLKRRPGEGPNPVGSGMEPPKAP 285
 QY 262 --PDVTVAVEETIPSTFGTSP 281
 Db 286 YFPDL-----VOPLPISGDVSP 303

RESULT 10
 TR6B_HUMAN
 ID TR6B_HUMAN STANDARD; PRT; 300 AA.
 AC 095407;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor, receptor superfamily member 6B precursor (Decoy
 receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).
 GN TNFRSF6B OR DCR3 OR TR6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal lung;
 RX MEDLINE=99087326; PubMed=9872321;
 RA Pitti R.M., Marsers S.A., Lawrence D.A., Roy M., Kischkel F.C.,
 RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
 RA Goddard P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
 RA "Genomic amplification of a decoy receptor for Fas ligand in lung and
 RT colon cancer.";
 RL Nature 396:699-703(1998).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
 RC TISSUE=Prostate;
 RX MEDLINE=99253915; PubMed=10318773;
 RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Dner R., Kwon B.S.;
 RT "A newly identified member of tumor necrosis factor receptor
 RL superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
 J. Biol. Chem. 274:13733-13736(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=20122600; PubMed=10655513;
 RA Bal C., Connolly B., Metzker M.L., Hiliard C.A., Liu X., Sandig V.,
 RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
 RT "Overexpression of M68/DCR3 in human gastrointestinal tract tumors
 RT independent of gene amplification and its location in a four-gene
 RT cluster.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Straube R.L., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usslin T.B., Toshlyuk S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerich A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC - FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT
 CC and TNFSF6/FasL. Protects against apoptosis.
 CC - SUBCELLULAR LOCATION: Secreted.
 CC TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
 CC Detected in adult stomach, spinal cord, lymph node, trachea,
 CC spleen, colon and lung. Highly expressed in several primary tumors
 CC from colon, stomach, rectum, esophagus and in SW480 colon
 CC carcinoma cells.
 CC - SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 CC -----
 DR EMBL; AF104419; AAD03056.1; -;
 DR EMBL; AF134240; AAD29688.1; -;
 DR EMBL; AF217796; AAF35244.1; -;
 DR EMBL; AF217793; AAF33685.1; -;
 DR EMBL; AF217794; AAF33686.1; -;
 DR EMBL; AL121845; CAC03668.1; -;
 DR EMBL; BC017065; AAH17065.1; -;
 DR EMBL; BC034349; AAH34349.1; -;
 DR HSSP; O14763; IDOG.
 DR Genew; HGNC:11921; TNFRSF6B.
 DR MIM; 603361; -;
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006916; P:anti-apoptosis; TAS.
 DR InterPro; IPR001368; TNFR_c6.
 DR SMART; SM00208; TNFR_c6; 4.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1
 FT CHAIN 30 300
 FT REPEAT 31 70
 FT REPEAT 72 113
 FT REPEAT 115 150
 FT REPEAT 152 193
 FT DISULFID 49 62
 FT DISULFID 52 70
 FT DISULFID 73 88
 FT DISULFID 91 105
 FT DISULFID 95 113
 FT DISULFID 115 126
 FT DISULFID 132 150
 FT DISULFID 153 168
 FT DISULFID 174 193
 FT CARBOHYD 173 173
 FT SEQUENCE 300 AA; 32679 MW; P90ABE337718449AF CRC64;
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Query Match 15.6%; Score 246; DB 1; Length 300;
 Best Local Similarity 35.4%; Pred. No. 1.1e-12;

NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93252381; PubMed=8486360;
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
 RT "Construction and evaluation of a hncDNA library of human 12p
 transcribed sequences derived from a somatic cell hybrid.";
 RL Genomics 16:214-218(1993).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cassavani T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [3]
 RP FUNCTION;
 RX MEDLINE=94225209; PubMed=8171323;
 RA Crowe P.D., Vanarsdale T.L., Walter B.N., Ware C.F., Hession C.,
 RA Ehrenfeld B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
 RT "A lymphotoxin-beta-specific receptor.";
 RL Science 264:707-710(1994).
 [4]
 RP CHARACTERIZATION;
 RX MEDLINE=99223511; PubMed=10207006;
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
 RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
 death in HeLa cells.";
 RL J. Biol. Chem. 274:11868-11873(1999).
 [5]
 RP FUNCTION;
 RX MEDLINE=20261554; PubMed=10799510;
 RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
 RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
 RT "The lymphotoxin-beta receptor is necessary and sufficient for
 LIGHT-mediated apoptosis of tumor cells.";
 RL J. Biol. Chem. 275:14307-14315(2000).
 [6]
 RP INTERACTION WITH TRAF3;
 RX MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RA Yagita H., Okumura K.;
 RT "TRAF3, an activator of NF-kappaB and putative signal transducer for
 the lymphotoxin-beta receptor.";
 RL J. Biol. Chem. 271:14661-14664(1996).
 [7]
 RP INTERACTION WITH TRAF4;
 RX PubMed=9626059;
 RA Krajewska M., Krajewski S., Zapata J.M., Vanarsdale T.,
 RA Gascoyne R.D., Berern K., McFadden D., Shabalak A., Hugh J.,
 RA Reynolds A., Cleveland C.V., Reed J.C.;
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
 adult, fetal, and tumor tissues.";
 RL Am. J. Pathol. 152:1549-1561(1998).
 [8]

RP INTERACTION WITH TRAF5.
 RX MEDLINE=98172745; PubMed=9511754;
 RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
 RA Otsuka M., Yamamoto T., Inoue J.-I.;
 RT "Cloning and characterization of a cDNA encoding the human homolog of
 tumor necrosis factor receptor-associated factor 5 (TRAF5).";
 RL Gene 207:135-140(1998).
 CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 LTA and LTB, and for TNFSF4/LIGHT. Promotes apoptosis via TRAF3
 and TRAF5. May play a role in the development of lymphoid organs.
 CC -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
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 CC
 CC EMBL; I04270; AAA6757.1; -
 CC EMBL; BC026262; AAH26262.1; -
 CC PIR; I54182; I54182.
 CC HSSP; P25942; ICDF.
 CC GENE; HGNC:6718; LTBR.
 CC MIM; 600979; -
 CC GO; 0007165; P:signal transduction; TMS.
 CC InterPro; IPR001368; TNFR_c6.
 CC Pfam; PF00020; TNFR_c6; 4.
 CC SMART; SM00208; TNFR; 4.
 CC PROSITE; PS00652; TNFR_NGFR_1; 2.
 CC PROSITE; PS00650; TNFR_NGFR_2; 3.
 CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 KW SIGNAL
 FT 1 435
 FT CHAIN
 FT 1 30
 FT DOMAIN 31 237
 FT TRANSMEM 228 248
 FT DOMAIN 249 435
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 168
 FT REPEAT 169 211
 FT REPEAT 212 255
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 73 80
 FT DISULFID 81 98
 FT DISULFID 99 116
 FT DISULFID 101 124
 FT DISULFID 125 142
 FT DISULFID 143 167
 FT DISULFID 168 185
 FT DISULFID 186 203
 FT CARBOHYD 40 45
 FT CARBOHYD 177 177
 SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CR64;
 Query Match 16.0%; Score 253; DB 1; Length 435;
 Best local Similarity 26.7%; Pred. No. 4.6e-13;
 Matches 86; Conservative 37; Mismatches 127; Indels 72; Gaps 16;
 QY 4 PG-DWGPPWRSTPRDVLRLVLYLTL-----GAPCYALRLPSCK--EDFY--PVGS 51
 DB 10 PGLAWCP-----LVILGLFGLAASQPAVPPVASENOTCRQGEKEYEPQHR 56
 QY 52 ECPCKSPGYRYKACGELTGVCEPCPGTYIAHLNGSKLCQCPAPGLASRNC 111
 DB 57 ICSSRCPPTTYSAKCSRIQDVTCATCAENSHNNTYITQLCPCPWGLEIAIC 116
 QY 112 STENAVCGCSQGHFCIVQGDHCAACRAYATSSPG-----QRYKGGTESODTLQNC 165

DE Soluble TNF receptor II precursor (cytokine response modifying protein
 DE B).
 GN CRM9 OR G2R OR GAR.
 OS Variola virus.
 CC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 CC Orthopoxvirus.
 OK NCBI_taxid=10255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=India-1967 / Isolate Ind3;
 RX MEDLINE=9320281; PubMed=8384129;
 RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
 RT "Genes of variola and vaccinia viruses necessary to overcome the host
 RT protective mechanisms.";
 RL FEBS Lett. 319:80-83(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bangladesh-1975;
 RX MEDLINE=94088747; PubMed=8264798;
 RA Maesung R.F., Esposito J.J., Liu L., Qi J., Uteerback T.R.,
 RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
 RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
 RA Venter C.J.;
 RT "Potential virulence determinants in terminal regions of variola
 RT smallpox virus genome.";
 RL Nature 366:748-751(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Garcia-1966, and Somalia-1977;
 RA Maesung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
 RA Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Garcia-1966;
 RX MEDLINE=20107289; PubMed=10639322;
 RA Shchelkunov S.N., Totmenin A.V., Loparev V.N., Safonov P.F.,
 RA Gutorov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Maesung R.F.,
 RA Esposito J.J.;
 RT "Alastrim smallpox variola minor virus genome DNA sequences.";
 RL Virology 266:361-386(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RT "DNA sequence analysis as a criterion for allocation of the
 RT orthopoxviruses to a particular species.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
 CC the modification of TNF-mediated antiviral processes (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X69198; CAA49137.1; -
 DR EMBL: X67117; CAA47540.1; -
 DR EMBL: L22579; AAA60933.1; -
 DR EMBL: U18339; AAA69407.1; -
 DR EMBL: U18341; AAA69467.1; -
 DR EMBL: Y16780; CAB54798.1; -
 DR EMBL: U88146; AAB94371.1; -
 DR EMBL: U88148; AAB94373.1; -
 DR EMBL: U88149; AAB94374.1; -
 DR EMBL: U88152; AAB94377.1; -
 DR PIR: D36858; D36858.

DR PIR: D72175; D72175.
 DR PIR: T28623; T28623.
 DR HSSP: O14763; 1D0G.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00650; TNFR_NGFR_2; 2.
 KW Receptor; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 349
 FT REPEAT 31 66
 FT REPEAT 67 108
 FT DISULFID 32 43
 FT DISULFID 44 57
 FT DISULFID 47 65
 FT DISULFID 68 83
 FT DISULFID 86 100
 FT DISULFID 90 108
 FT CARBOHYD 101 101
 FT CARBOHYD 173 173
 FT CARBOHYD 189 189
 FT CARBOHYD 215 215
 FT CARBOHYD 248 248
 FT VARIANT 17 17
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 FT VARIANT 165 165
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 FT VARIANT 274 274
 FT VARIANT 335 335
 FT VARIANT 339 339
 SQ SEQUENCE 349 AA; 38189 MW; D45D40B5C6E780BF CRC64;
 Query Match 16.3%; Score 257; DB 1; Length 349;
 Best Local Similarity 29.3%; Pred. No. 1.8e-13;
 Matches 66; Conservative 23; Mismatches 94; Indels 42; Gaps 8;
 QY 21 LRLVLYTFLGAPC-----YAPALPSCKDEYVSECCPKSPGVRVEACGEL 70
 DB 1 MKSLVYLYIFLSCIITINGDAAPYTPNKKCKDTEYKRNLCCLSPPTVYASRLCDCK 60
 QY 71 TGIVCEPCPPGTIAHLINGSKLQCO-MCDPAMGLPASRNCRTENAVGCGSPGHFCIV 129
 DB 61 TTNQCTPCGSGGTFTSRNNHLPACISGNGRCN--SNQVETRSCNTYHNRICEGSPGYCCL 118
 QY 130 QDDGHCAAGAYATSSPGQVQVKGCTESQTLQNCPPGTFS-----PNCITL 177
 DB 119 KGSAGCAKACVSOQKCGIGYGV-SGHTSVGVVICSPGFGYSHTVSSADKCEPVNPTFN 177
 QY 178 ECQ-----HOTKCSWLTKAGAGTSSSHWMMFISGLSVVI 214
 DB 178 YIDVETLYVNDTSCRTT---TGLSES-----ILTSLLITM 214
 RESULT 9
 TNFR3_HUMAN
 ID TNFR3_HUMAN STANDARD; PRT; 435 AA.
 AC P36941;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
 DE protein) (Tumor necrosis factor C receptor).
 GN LTRB OR TNFRSF3 OR TNFCR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RT urine. Evidence for immunological cross-reactivity with cell surface
 RT tumor necrosis factor receptors.";
 RL J. Biol. Chem. 265:11531-11536(1990).
 RN [8]
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE=91056048; PubMed=2173696;
 RA Loetscher H., Schlaepper E.J., Lahm H.-W., Pan Y.-C.E., Leselauer W.,
 RA Brochhaus M.;
 RA "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from H460 cells.";
 RT J. Biol. Chem. 265:20131-20138(1990).
 RN [9]
 RP CHARACTERIZATION.
 RX MEDLINE=93016040; PubMed=1328224;
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RA "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [10]
 RP INTERACTION WITH TRAF2.
 RX MEDLINE=94349371; PubMed=8069916;
 RA Roth M., Wong S.C., Henzel W.J., Goeddel D.V.;
 RA "A novel family of putative signal transducers associated with the
 RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
 RL Cell 78:681-692(1994).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
 RP TRAF2.
 RX MEDLINE=99221490; PubMed=10206649;
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
 RA "Structural basis for self-association and receptor recognition of
 RT human TRAF2.";
 RL Nature 398:533-538(1999).
 CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
 CC approximately 5-fold lower affinity for homotrimeric
 CC TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the
 CC apoptotic suppressors BIRC2 and BIRC3 to TNFSF1B/TNFR2.
 CC -1- SUBUNIT: Binds to TRAF2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
 CC -1- PTM: Phosphorylated; mainly on serine residues and with a very low
 CC level on threonine residues.
 CC -1- PTM: A soluble form (tumor necrosis factor binding protein 2) is
 CC produced from the membrane form by proteolytic processing.
 CC -1- PHARMACOLOGICAL: Available under the name Embrel (Immunex and
 CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid
 CC arthritis (RA). Embrel consist of the extracellular ligand-binding
 CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to
 CC TNF-alpha and blocks its interactions with receptors.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".
 CC -1- DATABASE: NAME=Embrel; NOTE=Clinical information on Embrel;
 CC WWW="http://www.embrel.com/".
 CC -----
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 CC -----
 CC EMBL; M33315; AAC59929.1; -;
 CC EMBL; US2165; AAC50622.1; -;
 CC EMBL; US2156; AAC50622.1; JOINED.
 CC EMBL; US2157; AAC50622.1; JOINED.
 CC EMBL; US2158; AAC50622.1; JOINED.
 CC EMBL; US2159; AAC50622.1; JOINED.
 CC EMBL; US2160; AAC50622.1; JOINED.
 CC EMBL; US2161; AAC50622.1; JOINED.
 CC EMBL; US2162; AAC50622.1; JOINED.

DR EMBL; US2163; AAC50622.1; JOINED.
 DR EMBL; US2164; AAC50622.1; JOINED.
 DR EMBL; M55994; AAA36755.1; -;
 DR EMBL; S61368; AAB19824.2; -;
 DR EMBL; M55857; AAA63262.1; -;
 DR EMBL; AB030950; BAA89053.1; -;
 DR PIR; A35356; A35356.
 DR PDB; 1CA9; 12-APR-99.
 DR Genew; HGNC:11917; TNFRSF1B.
 DR MIM; 191191; -;
 DR GO; GO:0005031; F.tumor necrosis factor receptor activity; TNS.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00208; TNFR_4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00650; TNFR_NGFR_2; 3.
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Phosphorylation; Pharmaceutical; Polymorphism; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 461
 FT FT
 FT CHAIN 27 2
 FT DOMAIN 23 257
 FT TRANSMEM 258 287
 FT DOMAIN 288 461
 FT REPEAT 39 76
 FT REPEAT 77 118
 FT REPEAT 119 162
 FT REPEAT 163 201
 FT DISULFID 40 53
 FT DISULFID 54 67
 FT DISULFID 57 75
 FT DISULFID 78 93
 FT DISULFID 96 110
 FT DISULFID 100 118
 FT DISULFID 120 126
 FT DISULFID 134 143
 FT DISULFID 137 161
 FT DISULFID 164 179
 FT CARBOHYD 171 171
 FT CARBOHYD 193 193
 FT CARBOHYD 196 196
 FT VARIANT 232 232
 FT VARIANT 141 141
 FT CONFLICT 363 363
 FT SEQUENCE 461 AA; 48291 MW; 603D0AE1CD69ACBF CRC64;
 Query Match 16.4%; Score 259; DB 1; Length 461;
 Best Local Similarity 32.8%; Pred. No. 1,6e-13;
 Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;
 QY 35 YAPALPS-CXEDBY--PVGSECCPKSPGYRVAECGELGTVCBPCPPGTYYIAHLNGHS 91
 DB 32 YAPBGSSTRLREHYDQTQMCSCSKSPGOHAKVFCTKTSIDVDCSCESTITQLMNVWP 91
 QY 92 KLIQCCWCDPAMGLRASRN-----CSRTENAVCGSPGHFCTVQDGDHCAACRAYATSS 145
 DB 92 ECLISC-----GSRSSDQVETQACTRBNRNICRTPGMVYALSKQEGCRICAPLRKCR 144
 QY 146 PQGRVXGCTESQDTLQCNCPGCTPS-PNGTLEBQCHQKRCMLVTKAGAG-----TSSS 199
 DB 145 PGFVARPPTETSDVCKPCAPGTFSTNTSDICRPHOICNVVAIPGNASMDAVCTSTS 204
 RESULT 8
 CRMB_VARY STANDARD; PRT; 349 AA.
 ID CRMB_VARY
 AC P34015; Q85407; Q89098; Q89118;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

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RX MEDLINE=87321103; PubMed=2820128;
RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RL telomeric region of the Shope fibroma virus genome.";
RN [2]
VN 160:20-30(1987).
RP FUNCTION.
RX MEDLINE=91207415; PubMed=1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RL McFadden G., Goodwin R.G.;
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
RL form of the TNF receptor.";
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPLIFY THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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CC -----
DR EMBL; M17433; -; NOT ANNOTATED_CDS.
DR EMBL; A23727; CA00167.1; -.
DR PTR; B43692; B43692.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KM Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT DISULFID 28 39 BY SIMILARITY.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 43 61 BY SIMILARITY.
FT DISULFID 64 79 BY SIMILARITY.
FT DISULFID 82 96 BY SIMILARITY.
FT DISULFID 86 104 BY SIMILARITY.
FT DISULFID 106 120 BY SIMILARITY.
FT DISULFID 123 146 BY SIMILARITY.
FT DISULFID 129 149 BY SIMILARITY.
FT DISULFID 164 185 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;
Query Match 16.5%; Score 260; DB 1; Length 325;
Best Local Similarity 31.5%; Pred. No. 9.5e-14;
Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

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Qy 180 ---QHQTCKSWLYTKAG 193
Db 177 LYPNERSCT---TTAG 190
RESULT 7
TRIM_HUMAN STANDARD; PRT; 461 AA.
AC P20333; Q16042; Q9UHN1;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Ectarecept)
DE [Contains: "Tumor necrosis factor binding protein 2 (TRPIL1)].
CN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90260635; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RL cellular and viral proteins.";
RL Science 248:1019-1023(1990).
[2]
RP SEQUENCE FROM N.A., AND VARIANT ARG-196.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RL naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299745; PubMed=8661109;
RA Beltzinger C.P., White P.S., Maris J.M., Salzman E.P., Jensen S.J.,
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.;
RL "Physical mapping and genomic structure of the human TNFR2 gene.";
RN Genomics 35:94-100(1996).
[4]
RP SEQUENCE OF 37-461 FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RL intracellular, domain sequences.";
RL Cytokine 2:231-237(1990).
[5]
RP SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
RX MEDLINE=90349572; PubMed=2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RL and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
[6]
RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21069356; PubMed=1197692;
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT "New single nucleotide polymorphisms in the coding region of human
RL TNFR2: association with systemic lupus erythematosus.";
RN Genes Immun. 1:501-503(2000).
[7]
RP SEQUENCE OF 27-31.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human

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RT the ligand binding domain of the human B cell receptor CD40.";
 RL Proteins 27:59-70(1997).
 RN [11]
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
 RX MEDLINE=98266353; PubMed=9605317;
 RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
 Zheng Z., Natsimh J.H., Thomas D.;
 RT "The role of polar interactions in the molecular recognition of CD40L
 with its receptor CD40.";
 RL Protein Sci. 7:1124-1135(1998).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
 RP TRAF3.
 RX PubMed=10984535;
 RA Ni C.Z., Welsh K., Leo E., Chion C.K., Wu H., Reed J.C., Ely K.R.;
 RT "Molecular basis for CD40 signaling mediated by TRAF3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
 RP TRAF3.
 RX PubMed=12005438;
 RA Li C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
 Satterthwait A.C., Cheng G., Ely K.R.;
 RT "Downstream regulator TRAF3 binds to the CD40 recognition site on
 TRAF3.";
 RL Structure 10:403-411(2002).
 RN [14]
 RP VARIANT HIGM3 ARG-83.
 RX MEDLINE=21532985; PubMed=11675497;
 RA Ferrati S., Gillani S., Insalaco A., Al-Ghonaime A., Soresina A.R.,
 Loubser M., Avanzini M.A., Marconi M., Badolati R., Ugazio A.G.,
 Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,
 Plebani A.;
 RT "Mutations of CD40 gene cause an autosomal recessive form of
 immunodeficiency with hyper IgM.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
 CC -1- FUNCTION: Receptor for TNFSFs/CD40L.
 CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 AND TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform I);
 CC secreted (isoform II).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=I;
 CC IsoId=P25942-1; Sequence=Displayed;
 CC Name=II;
 CC IsoId=P25942-2; Sequence=VSP_006472, VSP_006473;
 CC -1- TISSUE SPECIFICITY: B-cells and in primary carcinomas.
 CC -1- DISEASE: Defects in TNFRSF5 are the cause of type 3 hyper-IgM
 immunodeficiency (HIGM3), an autosomal recessive disorder which
 includes an inability of B cells to undergo isotype switching, one
 of the final differentiation steps in the humoral immune system,
 an inability to mount an antibody-specific immune response, and a
 lack of germinal center formation.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD40 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd40.htm".
 CC
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 DR EMBL; X60592; CA43045.1; -;
 DR EMBL; AL035662; CAC17670.1; -;
 DR EMBL; AJ300189; CAC29424.1; -;
 DR EMBL; BC012419; AAH12419.1; -;
 DR PIR; S04460; A60771.
 DR PDB; 1CDF; 01-APR-97.
 DR PDB; 1FLJ; 14-AUG-00.

DR PDB; 1LOA; 08-FEB-00.
 DR PDB; 1CZ2; 26-SEP-01.
 DR PDB; 1D00; 31-OCT-01.
 Query Match 17.0%; Score 267.5; DB 1; Length 277;
 Best Local Similarity 26.1%; Pred. No. 2e-14;
 Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;
 QY 20 VLRLVLYLTGAPCAVPAL-----PSCKDEYVPGSECCPKSPGYRVKACGLGTG 74
 Db 1 MRLPLQCVLMG--CLITAHNRPPTACRKYHILNSCCSLCPGKLVSDCTEFETE 58
 QY 75 CEPSPGTYIAHNLGSLKLCQCMCPAMGLASRNCRTENAVCGSPGHFCTVODGDH 134
 Db 59 CLPGESEFIDWNRETHCHQHKYCDPNLGLRVOQKQTSBTDITCTCEGMCN--TSEA 115
 QY 135 CAACRAATSTPGQAVQKGTESODTLCQNCPPGTF--PGNTLEECQHQTKCN--LVTK 191
 Db 116 CESCVLHRSCTPGVGVQIATGVSDTICECPGVGFSSNVSAREKCHPMTSCETKDLVQ 175
 QY 192 AGAGTSSHHWMMFLSGSLVIVVCSVGLICVKRKRPGDVVKVVSQRQEAEGE 251
 Db 176 Q-MTNKTDVVCQPDRLRALVVIPIIFGILFA-----ILVLVFIKKVAKKPTNK 225
 QY 252 ATVIEALQAPPDV-----TTVAVEBTI 273
 Db 226 AP--HPKQEPQELNFPDDLPGSNTAPVQETL 255
 RESULT 4
 TNRS_BOVIN STANDARD; PRT; 269 AA.
 ID ID 028203;
 AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE "Tumor necrosis factor receptor superfamily member 5 precursor
 (CD40L receptor) (B-cell surface antigen CD40) (Fragment)."
 GN TNFRSF5 OR CD40.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97281252; PubMed=9135560;
 RA Hirano A., Brown W.C., Estes D.M.;
 RT "Cloning, expression and biological function of the bovine CD40
 RT homologue: role in B-lymphocyte growth and differentiation in
 RT cattle.";
 RL Immunology 90:294-300(1997).
 CC -1- FUNCTION: Receptor for TNFSFs/CD40L.
 CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 AND TRAF6 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC
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 CC
 DR EMBL; U57745; AAC48710.1; -;
 DR HSSP; P25942; 1CDF.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00208; TNFR_4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.

DB 25 TCSDKQYLDHGGCCDDCQPSRLTSHCTALEKQCHPCDSCGSESAQWNRIRCHQRHCE 84
QY 101 PAMGLPASNRCSTRTENAVCGSPGHFCIVODGHCACRAVATSSPGQVQKGTSSQDT 160
DB 85 PNOGLFVKRGTAEADPTVCTCKEGQCHTSKD---CEACQHTPCICPGFVMEKATETDT 141
QY 161 LCONCPRTGTPNGTL-EECQHOTKS---WLVTAGAGTSSSHVWVFLSGSLVIVV 215
DB 142 VCHPCVGFSPNSOSLFKECYPTWSCEDKNLEVLQK---GTSQTNVICGLKSMRALVY 198
QY 216 CSTVGLIC-----VKR--RKPRGVVAVIVSVOKRQGEAGCVATIEALQAPPDVT 266
DB 199 PVMGLITLITFGVLYIKKVKVKKDKN--EMLPARRQDPQME-----DYGHNTA 249
QY 267 VAVEETI 273
DB 250 APVQETL 256
RESULT 3
ID TNR5 HUMAN STANDARD; PRT; 277 AA.
AC P25942; Q9BYU0;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 5 precursor
DE (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RX MEDLINE=2475341;
RX MEDLINE=89356608; PubMed=2475341;
RT "A B-lymphocyte activation molecule related to the nerve growth
RT factor receptor and induced by cytokines in carcinomas."
RL EMOB J. 8:1403-1410(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=21638749; PubMed=11780052;
RX Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RX Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RX Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RX Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RX Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RX Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RX Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RX Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RX Ellington A.G., Franklins C., Griffiths M.N.D., Gwilliam R., Garner P.,
RX Grafham D.V., Griffiths C., Griffiths A., Fraser A., French L., Grier P.,
RX Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RX Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RX Kay M.P., Kimberley A.M., King A., Knights A., Laird G., Lawlor S.,
RX Levesaith M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RX Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
RX Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RX Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RX Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RX Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhenko R., Sims S.,
RX Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RX Swann R.M., Syamamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RX Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RX Whitehead S.L., Whitteker P., Willey D.L., Williams L., Williams S.A.,
RX Wilmington L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RX Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM II).
RX MEDLINE=21177110; PubMed=1172023;
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
RT "Regulation of CD40 function by its isoforms generated through
RT alternative splicing."
RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM I).
RC TISSUE=ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uscid T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF, a relative of TRAF, in CD40 signaling."
RL Science 267:1494-1498(1995).
RN [6]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95129692; PubMed=7530216;
RA Sato T., Irie S., Reed J.C.;
RT "A novel member of the TRAF family of putative signal transducing
RT proteins binds to the cytosolic domain of CD40."
RL FEBS Lett. 358:113-118(1995).
RN [7]
RP INTERACTION WITH TRAF1, TRAF2, TRAF3 AND TRAF5.
RX PubMed=9718306;
RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
RA Kehry M.R.;
RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)
RT interactions: regulation of CD40 signaling through multiple TRAF
RT binding sites and TRAF hetero-oligomerization."
RL Biochemistry 37:11836-11845(1998).
RN [8]
RP INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754;
RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I., Azuma S., Kato K., Hirai M.,
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5)."
RL Gene 207:135-140(1998).
RN [9]
RP INTERACTION WITH TRAF6.
RX PubMed=9432981;
RA Kashinawa M., Shitakata Y., Inoue J.-I., Nakano H., Okazaki K.,
RA Okumura K., Yamamoto T., Nagaoka H., Takemori T.;
RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates
RT extracellular signal-regulated kinase (ERK) activity in CD40
RT signaling along a ras-independent pathway."
RL J. Exp. Med. 187:237-244(1998).
RN [10]
RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorek J., Aruffo A.;
RT "Construction and analysis of a detailed three-dimensional model of

ID	TNRS_MOUSE	STANDARD	PTI	289 AA.
AC	P27512; Q99NE0; Q99NE1; Q99NE2; Q99NE3;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDW40).			
GN	TNFRSF5 OR CD40.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RX	SEQUENCE FROM N.A. (ISOFORM I).			
RX	MEDLINE=92105763; PubMed=13703.5;			
RA	Torres R.M., Clark E.A.;			
RT	"Differential increase of an alternatively polyadenylated mRNA			
RL	species of murine CD40 upon B lymphocyte activation.";			
RN	J. Immunol. 148:620-626(1992).			
RN	[2]			
REV	REVISIONS.			
RC	STRAIN=BALB/c;			
RA	Torres R.M.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM I).			
RC	STRAIN=BALB/c; TISSUE=Liver;			
RX	MEDLINE=93094586; PubMed=1281194;			
RA	Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,			
RA	Howard M., Cockayne D.A.;			
RT	"Genomic structure and chromosomal mapping of the murine CD40 gene.";			
RL	J. Immunol. 149:3921-3926(1992).			
RN	[4]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS II; III; IV AND			
RP	V).			
RX	MEDLINE=21117110; PubMed=11172023;			
RA	Tone M., Tone Y., Fairchild P.D., Wykes M., Waldmann H.;			
RT	"Regulation of CD40 function by its isoforms generated through			
RT	alternative splicing.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).			
RN	[5]			
RP	INTERACTION WITH TRAF3.			
RX	MEDLINE=95194010; PubMed=7533327;			
RA	Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;			
RT	"Involvement of CRF1, a relative of TRAF, in CD40 signaling.";			
RL	Science 267:1494-1498(1995).			
RN	[6]			
RP	INTERACTION WITH TRAF5.			
RX	MEDLINE=96382484; PubMed=8790348;			
RA	Ishida T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Matnabe T.,			
RA	Yamamoto T., Inoue J.-I.;			
RT	"TRAF5, a novel tumor necrosis factor receptor-associated factor			
RT	family protein, mediates CD40 signaling.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).			
CC	-1- FUNCTION: Receptor for TNFRSF5/CD40L.			
CC	-1- SUBUNIT: Interacts with TRAF3 and TRAF5. Interacts with TRAF1,			
CC	TRAF2 AND TRAF6 (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I, III, IV			
CC	and V); Secreted (isoform II).			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=5;			
CC	Name=I;			
CC	IsoId=P27512-1; Sequence=Displayed;			
CC	Name=II;			
CC	IsoId=P27512-2; Sequence=VSP_006474, VSP_006475;			
CC	Name=III;			
CC	IsoId=P27512-3; Sequence=VSP_006477, VSP_006478;			
CC	Name=IV;			
CC	IsoId=P27512-4; Sequence=VSP_006479, VSP_006480;			
CC	Name=V;			
CC	IsoId=P27512-5; Sequence=VSP_006476;			

CC	- - SIMILARITY: Contains 4 TNFR-Cys repeats.
CC	-----
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CC	-----
DR	EMBL; M83132; AAB08705.1; -
DR	EMBL; M94126; AAA37404.1; -
DR	EMBL; M94129; AAA37404.1; JOINED.
DR	EMBL; M94128; AAA37404.1; JOINED.
DR	EMBL; M94127; AAA37404.1; JOINED.
DR	EMBL; AJ401387; CAC29427.1; -
DR	EMBL; AJ401388; CAC29428.1; -
DR	EMBL; AJ401389; CAC29429.1; -
DR	EMBL; AJ401390; CAC29430.1; -
DR	PIR; A46476; A46476.
DR	HSSP; P25942; ICDF.
DR	MGI; M8336; Tnfzf5.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF000020; TNFR_c6; 4.
DR	SMART; SMO0208; TNFR_4.
DR	PROSITE; PS00652; TNFR_NGFR.1; 1.
DR	PROSITE; PS50050; TNFR_NGFR.2; 4.
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KM	Alternative splicing.
FT	SIGNAL 1 19
FT	CHAIN 20 289
FT	DOMAIN 20 193
FT	TRANSMEM 194 215
FT	DOMAIN 216 289
FT	REPEAT 25 60
FT	REPEAT 61 103
FT	REPEAT 104 144
FT	REPEAT 145 187
FT	DISULFID 26 37
FT	DISULFID 38 51
FT	DISULFID 41 59
FT	DISULFID 62 77
FT	DISULFID 83 103
FT	DISULFID 105 119
FT	DISULFID 111 116
FT	DISULFID 125 143
FT	CARRHYD 153 153
FT	VARSPLIC 166 203
FT	
FT	
FT	
FT	VARSPLIC 204 289
FT	
FT	VARSPLIC 187 216
FT	
FT	VARSPLIC 216 234
FT	
FT	VARSPLIC 235 289
FT	
FT	VARSPLIC 216 222
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FT	VARSPLIC 223 289
FT	
SO	SEQUENCE 289 AA; 32111 MM; C79ICBD2FEA57AE CRC64;
Blast Match	Score 276.5; DB 1; Length 289;
Query Match	Similarity 27.9%; Pred. No. 4.1e-15;
Matches 69;	Conservative 43; Mismatches 106; Indels 29; Gaps 8
xy	41 SCKEBEYVGSECCPKSGPGYRVNEAGELGTGVCEPCPGTYIALNLGLASLCLOCOMCD 100

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RL [6]
 RN INTERACTION WITH TRAF2 AND TRAF5.
 RP PubMed=9153189;
 RX Heu H., Solovjev I., Colombero A., Elliott R., Kelley M., Boyle W.J.,
 RT "ATAR, a novel tumor necrosis factor receptor family member, signals
 RT through TRAF2 and TRAF5.";
 RL J. Biol. Chem. 272:13471-13474(1997).
 RN [7]
 RP INTERACTION WITH TRAF3 AND TRAF5.
 RX Masters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
 RA Ashkenazi A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
 RT "Herpesvirus entry mediator, a member of the tumor necrosis factor
 RT receptor (TNFR) family, interacts with members of the TNFR-associated
 RT factor family and activates the transcription factors NF-kappaB and
 RT AP-1.";
 RL J. Biol. Chem. 272:14029-14032(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
 RX MEDLINE=21403268; PubMed=11511370;
 RA Carli A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
 RA Eisenberg R.J., Wiley D.C.,
 RT "Herpes simplex virus glycoprotein D bound to the human receptor
 RT HxvD.";
 RL Mol. Cell 8:169-179(2001).
 CC -1- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
 CC TNFSF11/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
 CC an important role in HSV pathogenesis because it enhanced the
 CC entry of several wildtype HSV strains of both serotypes into CHO
 CC cells, and mediated HSV entry into activated human T cells.
 CC -1- SUBUNIT: INTERACTS WITH TRAF2, TRAF3 AND TRAF5.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (probable).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
 CC IN LUNG, SPLEEN, AND THYMUS.
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC -----
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 CC -----
 CC
 DR EMBL; U70321; AAB58354.1; -;
 DR EMBL; U81232; AAD00505.1; -;
 DR EMBL; AF153978; AAF75588.1; -;
 DR EMBL; AF373877; AAL47717.1; -;
 DR EMBL; AF373878; AAL47718.1; -;
 DR EMBL; BC002794; AAH02794.1; -;
 DR PDB; 1JMA; 26-SEP-01.
 DR Genew; HGNC:11912; TNFRSF14.
 DR MIM; 602746; -;
 DR GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR001368; TNFR_c6; 3.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.

DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
 KM 3D-structure.
 FT SIGNAL 1 38
 FT CHAIN 39 283
 FT
 FT DOMAIN 39 202
 FT TRANSMEM 203 223
 FT DOMAIN 224 223
 FT REPEAT 42 75
 FT REPEAT 78 119
 FT REPEAT 121 162
 FT DISULFID 42 53
 FT DISULFID 54 67
 FT DISULFID 57 75
 FT DISULFID 78 93
 FT DISULFID 96 111
 FT DISULFID 99 119
 FT DISULFID 121 138
 FT DISULFID 127 135
 FT CARBOHYD 110 110
 FT CARBOHYD 173 173
 FT VARIANT 17 17
 FT
 FT VARIANT 241 241
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 FT TURN 44 45
 FT STRAND 46 46
 FT STRAND 49 49
 FT TURN 50 51
 FT STRAND 52 52
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 FT STRAND 61 65
 FT STRAND 74 77
 FT TURN 80 81
 FT STRAND 82 83
 FT STRAND 88 88
 FT STRAND 94 95
 FT TURN 101 104
 FT STRAND 105 109
 FT STRAND 118 121
 FT TURN 123 124
 FT STRAND 125 129
 FT STRAND 137 140
 FT SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;
 SQ
 Query Match 99.8%; Score 1575; DB 1; Length 283;
 Best Local Similarity 99.6%; Pred. No. 1,7e-118;
 Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MBPPGDMGPPPPRSPTPTDVLRLVLYLFLGAPCAAPALPSCKEDEYPVGSCCPKCSFG 60
 DB 1 MBPPGDMGPPPPRSPTPTDVLRLVLYLFLGAPCAAPALPSCKEDEYPVGSCCPKCSFG 60
 QY 61 YRYKACGELTGTGVEPCPPGTIYIAHLNGLSKLCIQCMQDPMAGLPASNSCRTERAVCG 120
 DB 61 YRYKACGELTGTGVEPCPPGTIYIAHLNGLSKLCIQCMQDPMAGLPASNSCRTERAVCG 120
 QY 121 CSPGHFCIVQDDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSFNGTLEECQ 180
 DB 121 CSPGHFCIVQDDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSFNGTLEECQ 180
 QY 181 HQTCKSWLTKAGAGTSSHWVWPLSGSLVIVIVCSVTGLIICVRRKPRGDVVKYIVS 240
 DB 181 HQTCKSWLTKAGAGTSSHWVWPLSGSLVIVIVCSVTGLIICVRRKPRGDVVKYIVS 240
 QY 241 VQRKQGEAGEATVTEALQAPDVTTVAAVEETIPSTGSPNH 283
 DB 241 VQRKQGEAGEATVTEALQAPDVTTVAAVEETIPSTGSPNH 283

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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:27:40 ; Search time 17 Seconds

(without alignments)
782.856 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578

Sequence: 1 MEPPDWCPPWRSPTPTDV.....VTVAVEETIPSTGRSPNH 283

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5
Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1575	99.8	283	TR14_HUMAN	Q92956 homo sapien
2	276.5	17.5	289	TRN5_MOUSE	P27512 mus musculu
3	267.5	17.0	277	TRN5_HUMAN	P25942 homo sapien
4	267	16.9	269	TRN5_BOVIN	Q28203 bos taurus
5	266.5	16.9	349	CRMB_CAMPS	Q8UYA7 camelopox vi
6	260	16.5	325	VT2_SFVYA	P25943 Shope fibro
7	259	16.4	461	TR1B_HUMAN	P20333 homo sapien
8	257	16.3	349	CRMB_VARY	P34015 variola vir
9	253	16.0	435	TRR3_HUMAN	P34941 homo sapien
10	246	15.6	300	TRR3_HUMAN	O95407 homo sapien
11	245.5	15.6	415	TRR3_MOUSE	P50284 mus musculu
12	243.5	15.4	351	CRMB_COMPX	O73559 compox viru
13	240.5	15.2	271	TRR4_RAT	P15725 rattus norv
14	238.5	15.1	326	VT2_MXVVL	P25825 myxoma viru
15	236	15.0	332	TRR6_PIG	O77736 sus scrofa
16	215.5	13.7	272	TRR6_MOUSE	P47741 mus musculu
17	213.5	13.5	417	TR1B_MOUSE	Q940W1 mus musculu
18	213.5	13.5	474	TR1B_MOUSE	P25119 mus musculu
19	210	13.3	401	TR1B_HUMAN	O00300 homo sapien
20	209.5	13.3	616	TR11_HUMAN	Q9Y6Q6 homo sapien
21	206.5	13.1	324	TRR6_RAT	Q61199 rattus norv
22	206.5	13.1	417	TRR2_HUMAN	Q93038 h tumor nec
23	206	13.1	335	TRR6_HUMAN	P25445 homo sapien
24	205	13.0	327	TRR6_MOUSE	P25446 mus musculu
25	205	13.0	655	TR21_HUMAN	O75509 homo sapien
26	204	12.9	401	TR1B_MOUSE	O08712 mus musculu
27	203.5	12.9	425	TR16_RAT	P07174 rattus norv
28	201	12.7	401	TR1B_RAT	O08727 rattus norv
29	200.5	12.7	323	TRR6_BOVIN	P51867 bos taurus
30	198.5	12.6	416	TR16_CHICK	P18519 gallus galli
31	198.5	12.6	625	TR11_MOUSE	O35305 mus musculu
32	196	12.4	655	TR21_MOUSE	Q9EPU5 mus musculu
33	194.5	12.3	277	TRR4_HUMAN	P43489 homo sapien

34	192	12.2	461	TR1A_RAT	P22934 rattus norv
35	190	12.0	427	TR16_HUMAN	P08138 homo sapien
36	176.5	11.2	256	TRR9_MOUSE	P20334 mus musculu
37	173	11.0	498	TRR8_MOUSE	O60846 mus musculu
38	172.5	10.9	461	TR1A_PIG	P50555 sus scrofa
39	171.5	10.9	471	TR1A_BOVIN	O19131 bos taurus
40	171	10.8	250	TRR7_MOUSE	P41272 mus musculu
41	168.5	10.7	454	TR1A_MOUSE	P25118 mus musculu
42	168	10.6	176	TR23_MOUSE	O9E63 mus musculu
43	161	10.2	180	TR22_MOUSE	O9E62 mus musculu
44	161	10.2	255	TRR9_HUMAN	O07011 homo sapien
45	159	10.1	595	TRR8_HUMAN	P28908 homo sapien

ALIGNMENTS

RESULT 1
TR14_HUMAN STANDARD; PRT; 283 AA.
ID AC Q92956; Q8WXR1; Q96J31; Q9UM65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor
DE (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
DE (TR2).
GN TNFRSF14 OR HVEM OR HVFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervical adenocarcinoma;
RX MEDLINE=97053782; PubMed=8998196;
RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT the TNF/NGF receptor family.";
RL Cell 87:427-436(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97306336; PubMed=9162061;
RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-D.,
RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA Porter T.G., Truneh A., Young P.R.;
RT "A newly identified member of the tumor necrosis factor receptor
RT superfamily with a wide tissue distribution and involvement in
RT lymphocyte activation.";
RL J. Biol. Chem. 272:14272-14276(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Cao X.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.
RX MEDLINE=21629477; PubMed=11756979;
RA Struyf F., Posavac C.M., Keyaerts E., Van Ranst M., Corey L.,
RT "Search for polymorphisms in the genes for herpesvirus entry mediator,
RT Nectin-1, and Nectin-2 in immune seronegative individuals.";
RL J. Infect. Dis. 185:36-44(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,

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OY 50 GSECCPKSPGYRVKAEAGELTGV-----CEPCPG---TYIAHLNGLSKLOQOMCD 100
Db 56 GQFCHKPCPPGGRKARDC-----TVNGDEPDVCPCOEGKEYTDKAHFS--SKCRRCRLCD 108
OY 101 PAMGLRASRNCSTENAVCGSPGHFCIVQDGDHCAACRAVATSSPGQRVQKGTESQDT 160
Db 109 EGHGLEVEINCTRTONTKCRCKNFCC-----NST 138
OY 161 LCQNCPPGTFSFNGTLEEC--QHQTCSMLVTKAGAGTSSSHWWMFLSGSLVIVICST 218
Db 139 VCEHCDPCTKCEHGIKECTILTSNTKC-----KEGSRSNLGM-----LCLLLLP 183
OY 219 VGLICVRRKPRGDDVVIVIVSVQRKQOAEAGATVIEALQAPPDVTVAVEETIPSFYG 278
Db 184 IPLIWMVRKE-----VQTKCRKRKENQGSHEPTLNPEVAINLSDVDLSKYITTIAG 238
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Search completed: November 14, 2003, 17:32:18
Job time : 22 secs

Db 71 TSDTVACDCEASMYTQVMNQFRTCLSSCSSCTTDQVEIRA---CTKQNRVCACGAGRYC 127

QY 128 IYD-DGDHCAACRAVYATSSGQRYQKGTESQDTLCQNCPPGTF--PNGTLECCQHTQC 185

Db 128 ALKTHSGSCROCKRLKCGPGFVNASRPAENGVLCKACAPGTFSTSDVCRPHRIC 187

QY 186 SMLVTKAGAGTSS 198

Db 188 SIIAIPGNASTDA 200

RESULT 13

148854

gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C/Accession: 148854

R/Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.

Mamm. Genome 5, 726-727, 1994

A/Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.

A/Reference number: 148854; PMID:95178848; PMID:7873884

A/Accession: 148854

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-459 <RES>

A/Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831

C/Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

F:/151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 13.5%; Score 212.5; DB 2; Length 459;

Best Local Similarity 30.9%; Pred. No. 2, 8e-08;

Matches 46; Conservative 18; Mismatches 80; Indels 5; Gaps 4;

QY 53 CCEKSPGVRVKEACGELTGTCEPPEPTIYAHNLGSLKLCQC-QMCDPAMGLASRNC 111

Db 39 CCAKCPGQYVKKFKCNKTSPTVCADCEASMYTQVMNQFRTCLSSCSSC--STDQVETRAC 96

QY 112 SRPMNAVCGSPHFCTIQ-DGDHCAACRAVYATSSGQRYQKGTSSQDTLCQNCPPGTF 170

Db 97 TKQNRVVCACGAGRYATKALKHSGSCRCQKMLSLCGGFGVASSRAPNGVLCKACAPGTF 156

QY 171 S-PNGTLECCQHTKCSMLVTKAGAGTSS 198

Db 157 SDTTSSTDVCRPHRICSIIPAIGNASTDA 185

RESULT 14

JC2395

Fas antigen precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999

C/Accession: JC2395; PC2246

R/Kimura, K.; Wakatsuki, T.; Yamamoto, M.

Biochem. Biophys. Res. Commun. 198, 666-674, 1994

A/Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver

A/Reference number: JC2395; PMID:94128114; PMID:7507668

A/Accession: JC2395

A/Molecule type: mRNA

A/Residues: 1-324 <KIM>

A/Cross-references: DDBJ:D26112; NID:g468486; PIDN:BA05108.1; PID:d1005650; PID:g468487

A/Experimental source: thymus

A/Accession: PC2246

A/Molecule type: mRNA

A/Residues: 1-62, 'RPT' <K12>

A/Cross-references: DDBJ:D26113; NID:g468488; PIDN:BA05109.1; PID:d1005651; PID:g468489

A/Experimental source: liver

C/Genetics:

A/Intons: 62/1

C/Superfamily: NGF receptor repeat homology

C/Keywords: transmembrane protein

F:/1-21/Domain: signal sequence #status predicted <SIG>

F:/22-34/Product: Fas antigen #status predicted <MAT>

F:/4-79/Domain: NGF receptor repeat homology <NGF>

F:/81-124/Domain: NGF receptor repeat homology <NGA>

F:/171-188/Domain: transmembrane #status predicted <TM>

Query Match 13.1%; Score 206.5; DB 2; Length 324;

Best Local Similarity 24.7%; Pred. No. 5, 7e-08;

Matches 58; Conservative 27; Mismatches 93; Indels 57; Gaps 6;

QY 41 SCKEDBYPGSECCRCSPGVRVKEACGELTGT-VCEPPPG-TYIAHLGSLKLCQCM 98

Db 43 NCSBGLYGVPPFCQPCQGERKVKDCTTSGAPFCHPCTCEBEYDRKHYDKRCRCAP 102

QY 99 CDPAMGLASRNCSTENAVCGSPHFCTIVDDGHCAACRAVYATSSPGQRYQKGTESQ 158

Db 103 CDEGHLEVENCTRTQNTKCRCKENFYCNALCHCHYC-----TSCGLEDILPETRTS 158

QY 159 DPLCQNCPPGTFSPNGTLECCQHTKCSMLVTKAGAGTSSSHWVWFSLGSLYIVYVCT 218

Db 159 NTRCKK-----QSSNYKLMIL-----ILPGL 180

QY 219 VGLIICVRRKRGDVVKIVSVORRQBEAGATYIALQAPDVTVAVEETI 273

Db 181 AILFVFYIKR-----YRKROPGDESGIPESVPMNVSDVNLKTYI 222

RESULT 15

A40036

apoptosis-mediating surface antigen Fas precursor - human

N/Alternate names: surface antigen APO-1

C/Species: Homo sapiens (man)

C/Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000

C/Accession: A40036; S24543; A38142

R/Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Samehima, M.; Hase,

Cell 66, 233-243, 1991

A/Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can med.

A/Reference number: A40036; PMID:9109137; PMID:1713127

A/Accession: A40036

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-335 <ITO>

A/Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410

R/Kramer, P.H.

submitted to the EMBL Data Library, February 1992

A/Reference number: S24543

A/Accession: S24543

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-335 <KRA>

A/Cross-references: EMBL:X63717; NID:g28741; PID:g28742

R/Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Ricci,

J. Biol. Chem. 267, 10709-10715, 1992

A/Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member

A/Reference number: A38142; PMID:92268122; PMID:1375228

A/Accession: A38142

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-134, 'Q', 136-335 <OEH>

A/Experimental source: SKW6.4 cells

A/Note: sequence extracted from NCBI backbone (NCBIP:103810)

A/Note: in NCBI backbone the source is designated as mouse

C/Genetics:

A/Gene: GDB:APT1

A/Cross-references: GDB:132671; OMIM:134637

A/Map position: 10q24.1-10q24.1

C/Superfamily: NGF receptor repeat homology

C/Keywords: apoptosis; surface antigen; transmembrane protein

F:/1-16/Domain: signal sequence #status predicted <SIG>

F:/85-128/Domain: NGF receptor repeat homology <NGA>

F:/174-190/Domain: transmembrane #status predicted <TM>

Query Match 13.1%; Score 206; DB 2; Length 335;

Best Local Similarity 25.0%; Pred. No. 6, 4e-08;

Matches 60; Conservative 30; Mismatches 82; Indels 68; Gaps 9;


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RESULT 7
D36858
gene G4R protein - variola virus
M:Alternate names: B28R protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
A:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: D36858
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLU>
A:Cross-references: GB:X69198; NID:9456758; PIDN:CAA9137.1; PID:9457087
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Kolykhlov, A.A.; Blinov, V.M.; Gylorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Froil
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A:Reference number: S46868
A:Accession: S46888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <COL>
A:Cross-references: EMBL:X67117; NID:9516428; PIDN:CAA47540.1; PID:9516449
A:Experimental source: strain India-1967, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A:Reference number: S32385; MUID:93202281; PMID:8384129
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967, ssp. major
C:Gene: G4R
A:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:32-66/Domain: NGF receptor repeat homology <NGF>
F:68-109/Domain: NGF receptor repeat homology <NGF>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match
Best Local Similarity 16.3%; Score 257; DB 2; Length 349;
Matches 66; Conservative 23; Mismatches 94; Indels 42; Gaps 8;

QY 21 LRLVLYLFLGAPC-----YAPALPSCKEDYPVSGCCPKSPGYRVEKACGEL 70
DB 1 KMSVLYLYLFLSCIIINGRDAAPYPPNGKCKDTEYKRNHLCCLSCPGTYASRLCDSE 60
QY 71 TGTVEPCPPGTIYIAHLNLGSKLQCO-MCDPAMGLRASRNCSTENAVCGSPGHFCIV 129
DB 61 TWTQCTPCSGGTFTSNHNLPACTSCNGRCN--SNQVETRSCNTTHNRICECSPGYCYLL 118
QY 130 OQGDHCAACRAVATSPGQVOKGSGESQDTLCONCPPTFS-----PNGTLE 177
DB 119 KSSSGCKACVSOQTKGIGIV-SGHTSVQDVLCSPGFGTTHYVSSAKCEPVPNNNTN 177
QY 178 ECQ-----HQTCKSMVLVTRAGACTSSSHWVWFLSGSLVI 214
DB 178 YIDVEITLVVNDTCTRTT---TGLSES-----ILTSELITM 214

RESULT 8
154182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chalfanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A:Reference number: I54182; MUID:93252381; PMID:8486360

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A:Accession: I54182
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:L04270; NID:9339761; PIDN:AAA36757.1; PID:9339762
C:Gene: GDB:
A:Gene: GDB: LTR
A:Cross-references: GDB:1230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match
Best Local Similarity 16.0%; Score 253; DB 2; Length 435;
Matches 86; Conservative 37; Mismatches 127; Indels 72; Gaps 16;

QY 4 PG-DMGPPPMSTPTDVLRLVLYLFL-----GACPYALPSCK--EDFY--PVGS 51
DB 10 PGLAMGP-----LVTLGLFLGLAASQPAVPVYASQNTCRDQEKYVEPQHR 56
QY 52 ECCPCSPGYRKEACGELTVCPCPPGTIYIAHLNLGSKLQCOCDPAMGLRASNC 111
DB 57 ICCSRCPPTGYVSACSRIRDTVCATCENSYNEHWNTLTICLCRPPCDPVWGLEIAPC 116
QY 112 SRTENAVCGSPGHFCIVQDGDHCAACRAVATSPG-----QVOKGSGTESQDTLCONC 165
DB 117 TSKRKTQCRQCPGMFCAMW-ALECHHCELLSDCPGTEBELKDEVGKNNH-----CVPC 170
QY 166 PPGTF---SPNGTLEBCQHOTKC-SWLVTAGACTSSSHWVW-----FLSGSLVI 212
DB 171 KAGHPQNTSPSA--RCQPHTRCENQGLVEAPTAQSDTTCCKNPLEPLPPEMSGTMM 227
QY 213 VIVCSTVGLII-----CVKRRKRGDVVAVYVQKROAEAGATVIEALQAP---- 261
DB 228 LAVLLPLAPFLLATVFCIWKSHD--SLCKRLGSLKRRPGSGPPNVPAGSWEPKXAP 285
QY 262 --PDVTTVAVEETIPSTGRSP 281
DB 286 YFPDL-----VQPLPLPSGDVSP 303

RESULT 9
S12783
OX40 antigen precursor - rat
M:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12783; S08036
R:Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the mRC OX40 antigen of activated CD4 positive T lymphocyte
A:Reference number: S12783; MUID:90214614; PMID:2157591
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: EMBL:X17037; NID:9578330; PIDN:CAA34897.1; PID:957831
A:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-271/Product: OX40 antigen #status predicted <Mat>
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match
Best Local Similarity 15.2%; Score 240.5; DB 2; Length 271;
Matches 51; Conservative 16; Mismatches 54; Indels 25; Gaps 5;

QY 41 SCKEDYFVSGSCPKSPGYRKEACGELTVCPCPPGTIYIAHLNLGSKLQCOQMD 100
DB 25 NCVKTQYSGHKCKCEQCPGHGMVSRCHNTDTCHEPPEPGYNAVN-YDTCXQCTQCN 83
QY 101 PAMGLRASRNCSTENAVCGSPGHFCIVQDGDHCAACRAVATSPGQVOKGSGTESQDT 160
DB 84 HRSSEGLQNTCTPEDTVCOCRPG--TOPRODSSH-----KLGVVD----- 121

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A:Reference number: A36007, MUID:90349572, PMID:2166946
 A:Accession: A36007
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 116-140 'P', 142-195 'R', 197-362 'T', 364-461 <HEL>
 A:Cross-references: GB:M35857; NID:9339751; PIDN:AAA6362.1; PID:G339752
 R:Loetscher, H.; Schlaefer, E.O.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
 J. Biol. Chem. 265, 20131-20138, 1990
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor (TNF) isoforms
 A:Reference number: A23666; MUID:91056048; PMID:2173696
 A:Accession: A23666
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-40;65-69;136-141;300-306 <LOE>
 R:Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 15311-15316, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for a common binding site
 A:Reference number: A35010; MUID:90110215; PMID:2153136
 A:Accession: B35010
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-31 <ENG>
 R:Kuhnert, P.; Kemper, O.; Wallach, D.
 Gene 150, 381-386, 1994
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of the human TNF gene
 A:Reference number: I38094; MUID:95121934; PMID:7821811
 A:Accession: I38094
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-37 <RES>
 A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701
 C:Genetics:
 A:Gene: GDB:TNFR2
 A:Cross-references: GDB:125914; OMIM:191191
 A:Map position: 1p36.2-1p36.2
 A:Intons: 26/3
 A>Note: the list of introns is incomplete
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:22-46/Domain: signal sequence #status predicted <SIG>
 F:46-76/Domain: NGF receptor repeat homology <NG1>
 F:76-119/Domain: NGF receptor repeat homology <NG2>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>
 F:262-379/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>
 F:111/193/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 16.4%; Score 259; DB 1; Length 461;
 Best Local Similarity 32.8%; Pred. No. 1.1e-11;
 Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;

QY 35 YAPALPS-CRDEY--EVSGECPCPKSPGYRVKACGELTGTVCPCPGTYIAHLNGLS 91
 DB 32 YAPPPGSTRRLREYDQTAQWCKSCSPGQAKVFCRTKTDVTCDSCEDESYTQJMWVP 91
 QY 92 KCIQCQCMCDPAMGLRARN-----CSRTENAVGCGSPGHFCTVQDDDHCAACRAVATSS 145
 DB 92 ECLISC-----GSRCSDDVETQACTREONRICCTCPRGWYCALSKQEGRLCAPLRKR 144
 QY 146 PGORVOKGTGTSQDTLQNCPCPGTFS--PNTGLECQHQTKCSMLVTAKAG-----TSSS 199
 DB 145 PGGVAVRPGTETISIVVCKPAPGTFSTNTSSTDICRHOICNVVAIFGNASMAVCTSTS 204

RESULT 5
 T28623
 hypothetical protein G2R - variola major virus
 C:Species: variola major virus
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T28623
 R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Uterback, T.R.; Knight, J.C.; Aubin

Nature 366, 748-751, 1993
 A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
 A:Reference number: Z20488; MUID:94088747; PMID:8264798
 A:Accession: T28623
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-348 <NAS>
 A:Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60933.1; PID:9439102
 A:Experimental source: strain Bangladesh 1975
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 16.3%; Score 257.5; DB 2; Length 348;
 Best Local Similarity 29.5%; Pred. No. 1.2e-11;
 Matches 66; Conservative 23; Mismatches 94; Indels 41; Gaps 8;

QY 21 LRLVLYTLFLGAPC-----YAPALPSCKDEYEVSGECPCPKSPGYRVKACGELT 71
 DB 1 MKSVLYLYTLFLSCIIINGRDADAPYTPNGKCKDVKRHNLCCLSCPGTYASRLCDSKT 60
 QY 72 GTVCEPCPGTYIAHLNGLSKLQCO-MCDPAMGLRARNCSRTENAVGCGSPGHFCTVQ 130
 DB 61 NTQCTPGSGTFTSRNNHLPACLSGRCN--SNQVETRSCTTHNRICSGGYCLL 118
 QY 131 DGDHCAACRAVATSSPGQRYVKGSTESQDTLQNCPCPGTFS-----PNTGLEE 178
 DB 119 GSSGCKACVSGTKGIGYGV-SGHTSVGVICSPCGGTYSHTVSADKCEPVPNTFNY 177
 QY 179 CQ-----HOTKCSMLVTAKAGTSSSHVWVWFLSGSLVYI 214
 DB 178 IDVEITLYPVNDTSCTRTT--TGLSES-----ILTSELTITM 213

RESULT 6
 D27175
 G2R protein - variola minor virus (strain Garcia-1966)
 C:Species: variola minor virus
 C>Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
 C:Accession: D72175
 R:Shchelkunov, S.N.; Tolmenin, A.V.; Guorov, V.V.; Safonov, P.F.; Massung, R.F.; Lopa
 submitted to Genbank, March 1998
 A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
 A:Reference number: A72150
 A:Accession: D72175
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1348 <SHC>
 A:Cross-references: GB:Y16780; NID:95830555; PIDN:CAB54798.1; PID:95830759
 A:Experimental source: strain Garcia-1966
 C:Genetics:
 A:Gene: G2R
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 16.3%; Score 257; DB 2; Length 349;
 Best Local Similarity 29.3%; Pred. No. 1.3e-11;
 Matches 66; Conservative 23; Mismatches 94; Indels 42; Gaps 8;

QY 21 LRLVLYTLFLGAPC-----YAPALPSCKDEYEVSGECPCPKSPGYRVKACGELT 70
 DB 1 MKSVLYLYTLFLSCIIINGRDADAPYTPNGKCKDVKRHNLCCLSCPGTYASRLCDSK 60
 QY 71 TGVCEPCPGTYIAHLNGLSKLQCO-MCDPAMGLRARNCSRTENAVGCGSPGHFCTV 129
 DB 61 TNGCTPGSGTFTSRNNHLPACLSGRCN--SNQVETRSCTTHNRICSGGYCLL 118
 QY 130 QDGDHCAACRAVATSSPGQRYVKGSTESQDTLQNCPCPGTFS-----PNTGLEE 177
 DB 119 KSSGCKACVSGTKGIGYGV-SGHTSVGVICSPCGGTYSHTVSADKCEPVPNTFNY 177
 QY 178 ECQ-----HOTKCSMLVTAKAGTSSSHVWVWFLSGSLVYI 214
 DB 178 YIDVEITLYPVNDTSCTRTT--TGLSES-----ILTSELTITM 214

Db 199 PVVMGILITIFGVELYIKVKVKPKDN--EMLPPARQDPQDME-----DYPGHNTA 249
 QY 267 VAVEETI 273
 Db 250 APVOETL 256

RESULT 2

B-cell activation protein CD40 precursor - human
 N/Alternate names: B-cell surface antigen Bp50
 C/Species: Homo sapiens (man)
 C/Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #ext_change 21-Jul-2000
 C/Accession: S04460; A60771
 R/Stamenkovic, I.; Clark, E.A.; Seed, B.
 EMBL J. 8, 1403-1410, 1989
 A/Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
 A/Reference number: S04460; MUID:89356608; PMID:2475341
 A/Accession: S04460
 A/Molecule type: mRNA
 A/Residues: 1-277 <STA>
 A/Cross-References: EMBL:X60592; NID:929850; PID:CAA43045.1; PID:929851
 R/Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A/Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
 A/Reference number: A60771; MUID:89093941; PMID:2463309
 A/Accession: A60771
 A/Molecule type: protein
 A/Residues: 21-50 <BRA>
 A/Experimental source: Burkitt lymphoma cell line Raji
 C/Genetic8:
 A/Genes: GDB:CD40
 A/Cross-References: GDB:215268; OMIM:109535
 A/Map position: 20q12-20q13.2
 C/Superfamily: CD27 antigen; NGF receptor repeat homology
 C/Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
 F.1-20/Domain: signal sequence #status predicted <SIG>
 F.21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
 F.21-193/Domain: extracellular #status predicted <EXT>
 F.216-215/Domain: transmembrane #status predicted <TM>
 F.216-277/Domain: intracellular #status predicted <CYT>
 F.153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.0%; Score 267.5; DB 2; Length 277;
 Best Local Similarity 26.1%; Pred. No. 1.8e-12;
 Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

QY 20 VRLVLYTLFLGAPCYAPALP-----SCKEDYFVSGCCPKCSPGYRVKACGELTGT 74
 Db 1 MRLPLQCVLMG--CLITVHPPPTACREKQYLINSQCCSLCOPQKLVSDCTETETE 58
 QY 75 CEPCEPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCGCSPGHFCIVODG 134
 Db 59 CLPCGSESLFTWNRRETHCHQHKYCDPNGLRVQKGTSETDITCCEBGWMC---TSDA 115
 QY 135 CAACRAVATSSPCQRVQKGTESQDPLCQNCPPGTSS--ENGTLBECQHOTKSW--LYTK 191
 Db 116 CESSCVLRSCSPGFGVQKQIATGVSDICPCPVGFSNVSASFEEKCHPTSCETKDLVQ 175
 QY 192 AGAGTSSSHWMMWFLSGSLVIYVCGSTVGILICVKRRKRGDVVKYIVGVRKQRAE 251
 Db 176 Q-AGNKIVVCGPDRRLALVIRPIIFGLRA-----ILLVLYIKVAKKPTNK 225
 QY 252 ATVTEALQAPPDV-----TTVAVEETI 273
 Db 226 AP--HPKQEPQEIFPDDPGSNTAPVQETL 255

RESULT 3
 B43692
 T2 protein - rabbit fibroma virus
 C/Species: rabbit fibroma virus, Shope fibroma virus
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #ext_change 07-May-1999

C/Accession: B43692
 R/Upton, C.; Delange, A.M.; McFadden, G.
 Virology 160, 20-30, 1987
 A/Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
 A/Reference number: A43692; MUID:87321103; PMID:2820128
 A/Accession: B43692
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-325 <UPR>
 A/Cross-References: GB:M17433
 C/Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 F.64-105/Domain: NGF receptor repeat homology <NG2>
 F.106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 16.5%; Score 260; DB 2; Length 325;
 Best Local Similarity 31.5%; Pred. No. 7.3e-12;
 Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VRLVLYTLFLGAPCYAPALP-----SCKEDYFVSGCCPKCSPGYRVKACGELTGT 73
 Db 1 MRLPLQCVLMG--CLITVHPPPTACREKQYLINSQCCSLCOPQKLVSDCTETETE 59
 QY 74 CEPCEPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCGCSPGHFCIVODG 132
 Db 60 VCSPEDEGTFSTAHAPACVSCR--GCTGHLSSQPCDRTDRVCNCSGTNYCLKQ 117
 QY 133 DHCAACRAVATSSPCQRVQKGTESQDPLCQNCPPGTSSPN--GTLEEC----- 179
 Db 118 NCRIC-APQTCPCPAGYGVSGHTRAGDILCEKCPHTYSDLSPTERCSTFNYSVGFN 176
 QY 180 ---OHQTKCSMLVTKAG 193
 Db 177 LYPVNETCT---TTAG 190

RESULT 4

A35356
 tumor necrosis factor receptor 2 precursor [validated] - human
 N/Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 08-Dec-2000
 C/Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
 R/Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.
 Science 248, 1019-1023, 1990
 A/Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
 A/Reference number: A35356; MUID:90260639; PMID:2160731
 A/Accession: A35356
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-461 <SMI>
 A/Cross-References: GB:M23315; NID:9189185; PID:AAA59929.1; PID:9189186
 R/Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
 Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A/Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
 A/Reference number: A36475; MUID:91045991; PMID:2172983
 A/Accession: A36475
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-195, 'R', 197-461 <KOH>
 A/Cross-References: GB:M55994; GB:M8549; NID:9339757; PID:AAA36755.1; PID:9339758
 R/Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
 Cytokine 2, 231-237, 1990
 A/Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
 A/Reference number: A48416; MUID:91370690; PMID:1966549
 A/Accession: A48416
 A/Status: preliminary
 A/Molecule type: mRNA; protein
 A/Residues: 23-461 <DEM>
 A/Cross-References: GB:S63368; NID:9235648; PID:AAA19824.1; PID:9235649
 A/Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:P:63371)
 R/Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A/Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra

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RESULT 15

AA05797 standard; Protein; 283 AA.

AA05797;

02-AUG-1999 (first entry)

Herpes virus entry mediator (HVEM).

Herpes virus entry mediator; HVEM, HSV receptor; infection; diagnosis; therapy; vaccine; antiviral; assay.

Human herpes simplex virus.

MO9920761-A2.

29-APR-1999.

22-OCT-1998; 98WO-US22342.

22-OCT-1997; 97US-0955531.

(UNMI) UNIV MICHIGAN.

Fuller AO, Li Q, McLaren NC, Perez A, Subramanian G;

WPI: 1999-302740/25.

N-PSDB; AAX25512.

Human herpes simplex virus receptor B5 and HVEM compositions

Claim 10; Page 71-72; 89pp; English.

The present sequence represents HVEM, a novel human herpes simplex virus (HSV) entry mediator that is a member of the tumour necrosis factor receptor family, and which confers on HSV the ability to infect and replicate in otherwise non-permissive cells. In the present invention, the combination of a novel porcine cell model system which is refractory to HCV entry, along with specific HSV B5 (see AA05796) and/or HVEM receptor proteins enables the development of assays for screening antiviral compounds and therapeutics. The assays are useful for detecting the ability of agents to inhibit CC HSV entry or spread and provide for facile high-throughput screening of compounds suspected to be able to inhibit such entry, e.g. compound libraries, peptide libraries etc., to identify potential drug candidates. The invention also provides a vaccine comprising the HSV receptor, an immunogenic polypeptide or fragments of the polypeptide.

SQ Sequence 283 AA;

Query Match 99.5%; Score 1570; DB 20; Length 283;

Best Local Similarity 99.3%; Pred. No. 5.9e-120; Mismatches 1; Indels 0; Gaps 0;

Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDYFVGSCECPKCSPG 60

DB 1 MEPPGDMGPPWRSTPRTDVLRVLVLTFLGAPCYAPALPSCKEDYFVGSCECPKCSPG 60

QY 61 YRVKACGELTGTVCPCPTGYIAHLNGLSKLCQCOMCDPAMGLRASRNCRTENAFCG 120

DB 61 YRVKACGELTGTVCPCPTGYIAHLNGLSKLCQCOMCDPAMGLRASRNCRTENAFCG 120

QY 121 CSPGHFCIVDDGHCACRAVATSSPGQVQKGTESQDTLCQNCPPGTSPNGTLEECQ 180

DB 121 CSPGHFCIVDDGHCACRAVATSSPGQVQKGTESQDTLCQNCPPGTSPNGTLEECQ 180

QY 181 HQTKCSWLVTYKAGTSSSHWMMFLSGSLVIVIVCSTVGLITCVKRRKPRGDVVKIVS 240

DB 181 HQTKCSWLVTYKAGTSSSHWMMFLSGSLVIVIVCSTVGLITCVKRRKPRGDVVKIVS 240

QY 241 VQRKQAEAGATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
DB 241 VQRKQAEAGATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

Search completed: November 14, 2003, 17:30:21
Job time : 42 secs

PT useful for treating stroke, Alzheimer's disease and AIDS
 XX Disclosure; Page 13-14; 18pp; English.
 CC The invention relates to identifying agonists or antagonists to tumour
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TR2
 CC and TR4). The method comprises: (a) (i) contacting TR1 or TR2 with a
 CC candidate compound in the presence of TR2 or TR4; or (ii) contacting TR2
 CC or TR4 with a candidate compound in the presence of TR1 or TR2; and (b)
 CC assessing the ability of the candidate compound to compete with TR1 or
 CC TR2 binding to TR2 or TR4. TR and TR agonists and antagonists are useful
 CC for treating diseases caused by imbalance of TR or TR polypeptide levels,
 CC which cause: chronic and acute inflammation, arthritis, septicemia,
 CC autoimmune diseases, transplant rejection, graft vs. host disease,
 CC infection, stroke, ischemia, acute respiratory disease syndrome,
 CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis
 CC and Alzheimer's disease. The present sequence represents a TNF-R related
 CC polypeptide TR2.
 CC
 SQ Sequence 283 AA:
 Query Match 99.6%; Score 1572; DB 20; Length 283;
 Best Local Similarity 99.6%; Pred. No. 4.1e-120;
 Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MEPPGDMGPPPPRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSFG 60
 DB 1 MEPPGDMGPPPPRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSFG 60
 QY 61 YVKEACGELTGTCPCPPGTIAHLNGLSKLCLOCCMDPAMGLRASNCRSTENAVCG 120
 DB 61 YVKEACGELTGTCPCPPGTIAHLNGLSKLCLOCCMDPAMGLRASNCRSTENAVCG 120
 QY 121 CSPGHFCTIVODGDHCAACRAVATSSPGQVOKGTESQDTLCONCPGTFSPNGTLEBCQ 180
 DB 121 CSPGHFCTIVODGDHCAACRAVATSSPGQVOKGTESQDTLCONCPGTFSPNGTLEBCQ 180
 QY 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIYS 240
 DB 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIYS 240
 QY 241 VORKROEAGEATVIEALQAPDPVTTVAEETIPSTGSPNH 283
 DB 241 VORKROEAGEATVIEALQAPDPVTTVAEETIPSTGSPNH 283
 RESULT 14
 ID AAM12659
 AA12659 standard; Protein; 283 AA.
 AC AAM12659;
 XX
 DT 07-MAY-1997 (first entry)
 XX
 DE Human herpes simplex virus cellular mediator.
 XX
 KW Herpes simplex virus cellular mediator; HVEM; receptor; HSV;
 XX diagnosis; agonist; antagonist; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..38
 FT /label= Sig_peptide
 FT Protein 39..283
 FT /label= Mat_protein
 FT Region 42..75
 FT /note= "cysteine-rich repeat characteristic of
 FT TNF/NGF receptor family"
 FT Region 76..120
 FT /note= "cysteine-rich repeat characteristic of
 FT TNF/NGF receptor family"
 FT Region 121..162

FT /note= "cysteine-rich repeat characteristic of
 FT TNF/NGF receptor family"
 FT Region 163..185
 FT /note= "partial cysteine-rich repeat characteristic
 FT of TNF/NGF receptor family"
 FT Domain 203..225
 FT /label= Transmembrane_domain
 FT Modified-site 110..112
 FT /label= Glycosylation
 FT /note= "potential N-glycosylation site"
 FT Modified-site 173..175
 FT /label= Glycosylation
 FT /note= "potential N-glycosylation site"
 PN MO9704658-A1.
 XX
 PD 13-FEB-1997.
 XX
 PF 26-JUL-1996; 96WO-US12374.
 XX
 PR 28-JUL-1995; 95US-0509024.
 XX
 PA (NOUN) UNIV NORTHWESTERN.
 XX
 PI Montgomery RI, Spear PG;
 DR WPI, 1997-145273/13.
 XX
 DR N-PSDB; AAT51737.
 PT New human herpes simplex virus cellular mediator - used for
 PT diagnosis, drug screening and therapeutically to inhibit entry of
 PT HSV into cells
 XX
 PS Claim 1; Fig 2; 54pp; English.
 XX
 PS Human herpes simplex virus (HSV) cellular mediator (HVEM) (AAM12659)
 CC is a novel member of the TNF/NGF receptor family that mediates or
 CC enhances entry of HSV into cells. Its amino acid sequence was
 CC deduced from a cDNA clone (AAT51737) isolated from an HeLa library
 CC by its ability to convert CHO-K1 cells from resistance to
 CC susceptibility to HSV-1 entry. Recombinant HVEM can be produced in
 CC bacterial or mammalian (esp. CHO) cells. It can be used as an
 CC immunosay reagent to detect specific antibodies, to screen for
 CC drugs having an (ant)agonist effect on HSV entry into cells, to
 CC generate antibodies, to screen for the (currently unknown) HVEM
 CC ligand, and to identify inhibitors of HSV-HVEM interaction.
 CC
 SQ Sequence 283 AA:
 Query Match 99.5%; Score 1570; DB 18; Length 283;
 Best Local Similarity 99.3%; Pred. No. 5.9e-120;
 Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MEPPGDMGPPPPRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSFG 60
 DB 1 MEPPGDMGPPPPRSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSFG 60
 QY 61 YVKEACGELTGTCPCPPGTIAHLNGLSKLCLOCCMDPAMGLRASNCRSTENAVCG 120
 DB 61 YVKEACGELTGTCPCPPGTIAHLNGLSKLCLOCCMDPAMGLRASNCRSTENAVCG 120
 QY 121 CSPGHFCTIVODGDHCAACRAVATSSPGQVOKGTESQDTLCONCPGTFSPNGTLEBCQ 180
 DB 121 CSPGHFCTIVODGDHCAACRAVATSSPGQVOKGTESQDTLCONCPGTFSPNGTLEBCQ 180
 QY 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIYS 240
 DB 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIYS 240
 QY 241 VORKROEAGEATVIEALQAPDPVTTVAEETIPSTGSPNH 283
 DB 241 VORKROEAGEATVIEALQAPDPVTTVAEETIPSTGSPNH 283

AC	AAV94717;
XX	
DT	29-JAN-2001 (first entry)
XX	
DE	Human TR2-receptor protein sequence.
XX	
KW	Tumour necrosis factor-receptor related protein; TR2; human; cancer;
KW	chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
KW	immunodeficiency; metastasis; hemolytic anaemia; actinia; X-linked SCID;
KW	severely combined immunodeficiency; apoptosis inhibition;
XX	Alzheimer's disease; Parkinson's disease; Crohn's disease.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Location/Qualifiers
FT	Peptide
FT	1..36
FT	/note= "Signal peptide"
FT	Protein
FT	37..283
FT	/label= "TR2 receptor"
FT	Domain
FT	37..200
FT	/note= "Extracellular domain"
FT	Domain
FT	201..225
FT	/note= "Transmembrane domain"
FT	Domain
FT	226..283
FT	/note= "Intracellular domain"
XX	
PN	WO200056405-A2.
XX	
PD	28-SEP-2000.
XX	
PF	22-MAR-2000; 2000WO-US07521.
XX	
PR	22-MAR-1999; 99US-0125683.
PR	26-MAR-1999; 99US-0126522.
PR	20-MAY-1999; 99US-0135169.
PR	06-AUG-1999; 99US-0147383.
XX	
PA	(NIJ/) NI J
PA	(ROSE/) ROSEN C A.
PA	(GENTZ/) GENTZ R L.
XX	
PI	NI J, Rosen CA, Gentz RL;
XX	
DR	WPI; 2000-594519/56.
XX	
DR	N-PSDB; AAA28135.
XX	
PT	Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
PT	and its two splice variants, useful for treating arthritis or
PT	inflammation, cancer (such as follicular lymphomas) and
PT	immunodeficiency disorders.
XX	
PS	Claim 1; Fig 1; 373pp; English.
XX	
CC	This invention relates to an isolated nucleic acid molecule encoding a
CC	human tumor necrosis factor (TNF)-receptor related protein TR2. Included
CC	in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
CC	The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a
CC	member of the TNFR superfamily. The invention includes a method for the
CC	treatment of arthritis or inflammation using an antibody directed against
CC	a fragment of the TR2 protein. TR2 its agonists, antagonists and
CC	antibodies exhibit cytostatic, dermatological, antineoplastic,
CC	immunopressive, antiallergic, antiarthritic, antiaesthetic,
CC	antiinflammatory, neuroprotective, nootropic, antiparkinsonian, and
CC	cerebroprotective activity. The methods are useful for treating arthritis
CC	or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
CC	mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
CC	immunodeficiency or for enhancing an in vivo leukocyte response to an
CC	antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
CC	preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
CC	dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
CC	inflammatory myopathies) and immunodeficiency disorders (such as severely
CC	combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
CC	disorder, or Neelof syndrome-combined immunodeficiency with 19s). TR2,

	CC	TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or antagonists are useful for treating or preventing autoimmune diseases and inhibit the growth, progression and/or metastasis of cancers. They are also used to activate, differentiate or proliferate cancerous cells or tissue, and can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, e.g. Alzheimer's disease.
	CC	Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful as sources for generating antibodies, as molecular weight markers.
	CC	This sequence represents the TR2 receptor protein of the invention.
	XX	
SQ	Sequence	283 AA;
Query Match	99.8%; Score 1575; DB 21; Length 283;	
Best Local Similarity	99.6%; Pred. No. 2.3e-120;	
Matches	282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
OY	1 MEPPGDMGPPEWRSTPRTDVLRLVLYTLFLGAPCYAPALPSCKEDFVPVSGCCPKCSPG 60	
DB	1 MEPPGDMGPPEWRSTPRTPKTDVLRLLVLTFLGAPCYAALPSCKDDEFPVSGCCPKCSPG 60	
OY	61 YRVKACGELTGIVCEPCPEGTYYIAHLNGLSKLQCCMPAMGLRASRNCRTENAVCG 120	
DB	61 YRVKACGELTGIVCEPCPEPTYYIAHLNGLSKLQCCMPAMGLRASRNCRTEMVCG 120	
OY	121 CSPHFICITVDGDHCACRAVAATSSPQRQXQKGTESDTLCONCPGETSPNGTLEECQ 180	
DB	121 CSPHFICITVDGDHCAACRAVAATSSPQARVQKGTESDTLCONCPGETSPNGTLEECQ 180	
OY	181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIYVCSTVGLIICVKRRKPGRGVKKYIVS 240	
DB	181 HQTCSMLVTKAGAGTSSSHHWMMFLSGSLVIYVCSTVGLIICVKRRKPGRGVKKYIVS 240	
OY	241 VORRKQEAEGEATVIEALQAPPDVTTVAVEETIPSTFGRSBNH 283	
DB	241 VORRKQAEAGEATVIEALQAPPDVTTVAVEETIPSTFGRSBNH 283	
RESULT 13		
ID	AAM95031 standard; protein; 283 AA.	
AA	AAM95031;	
DT	13-MAY-1999 (first entry)	
DE	Tumour necrosis factor receptor (TNF-R) related polypeptide TR2.	
XX		
KM	Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis; inflammation; septicemia; autoimmune disease; transplant rejection; graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS; acute respiratory disease syndrome; restenosis; bone disease; cancer; atherosclerosis; Alzheimer's disease.	
XX		
OS	Unidentified.	
XX		
PN	EP897114-A2.	
PD	17-FEB-1999.	
XX		
PF	04-JUN-1998; 98EP-0304424.	
XX		
PR	29-AUG-1997; 97US-0057550.	
PR	13-AUG-1997; 97US-0055513.	
XX	26-AUG-1997; 97US-0056980.	
PA	(SMIK) SMITHKLIN BEECHAM CORP.	
XX		
PI	Brigham-Burke MR, Young PR;	
DR	WPI; 1999-134308/12.	
TT	Identifying agonists and antagonists to tumour necrosis factor receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) -	

```
FT Domain 201..225
FT /note="Transmembrane domain"
FT Domain 226..283
FT /note="Intracellular domain"
XX WO9818824-A1.
XX PD 07-MAY-1998.
XX PF 30-OCT-1996; 96WO-US18540.
XX PR 30-OCT-1996; 96WO-US18540.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX PI Gentz RL, Hurle MR, Lyn SDP, Ni J, Rosen CA;
XX WPI; 1998-272139/24.
XX DR N-PSDB; AAV34509.
XX PT Nucleic acid encoding TR2 tumour necrosis factor family receptor -
XX PT and its splice variants, useful for diagnosis and treatment of
XX PT diseases involving abnormal cell survival or death, e.g. herpes
XX PT simplex infection
XX PS Claim 1; Fig 1; 151pp; English.
XX CC The human tumour necrosis factor (TNF) receptor related protein (TR2) is
XX CC a member of the TNF family and displays considerable homology to murine
XX CC CD40. It can be used in soluble forms to treat herpes simplex virus
XX CC infection and TR2 proteins (or their agonists or antagonists) are used to
XX CC treat disease associated with aberrant cell survival. Agonists may also
XX CC be used to protect against the effects of radiation therapy and to
XX CC stimulate lymphocyte proliferation and differentiation in patients
XX CC infected by human immune deficiency syndrome.
XX CC
XX CC Sequence 283 AA:
SQ
XX Query Match 99.8%; Score 1575; DB 19; Length 283;
XX Best Local Similarity 99.6%; Pred. No. 2.3e-120;
XX Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPPGDMGPPPMRSTPRDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
DB 1 MEPPGDMGPPPMRSTPRDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
QY 61 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCOMCDPAMGLRASRNCSTRTENAVCG 120
DB 61 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCOMCDPAMGLRASRNCSTRTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESDTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESDTLCONCPGTFSPNGTLEECQ 180
QY 121 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCOMCDPAMGLRASRNCSTRTENAVCG 120
DB 121 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCOMCDPAMGLRASRNCSTRTENAVCG 120
QY 181 HQTCKSMVLTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKRPBGDVVAVIYS 240
DB 181 HQTCKSMVLTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKRPBGDVVAVIYS 240
QY 241 VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
DB 241 VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
XX
XX RESULT 11
XX ID AAM87591
XX AA AAM87591 standard; Protein; 283 AA.
XX AC AAM87591;
XX XX
XX DT 17-MAR-1999 (first entry)
XX XX
XX DE Human tumour necrosis factor receptor-like 2 protein.
```

```
XX XX
XX Tumour necrosis factor receptor-like 2; TR2; TNF; human; psoriasis;
XX systemic lupus erythematosus; idiopathic thrombocytopenic purpura;
XX rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
XX insulin-dependent diabetes mellitus; allergic disorder; cancer; therapy;
XX atherosclerosis; viral infection.
XX OS Homo sapiens.
XX WO9851346-A1.
XX PD 19-NOV-1998.
XX PF 12-MAY-1998; 96WO-US09744.
XX PR 12-MAY-1997; 97US-0046249.
XX PA (SMK ) SMITHKLINE BEECHAM CORP.
XX (SMK ) SMITHKLINE BEECHAM PLC.
XX PI Harrop JA, Holmes SD, Reddy MP, Truneh A;
XX WPI; 1999-059689/05.
XX DR N-PSDB; AAV83763.
XX PT Method of treating pathological condition - comprises administering
XX PT tumour necrosis factor-2 antibody to patient
XX PS Disclosure; Page 27-28; 35pp; English.
XX CC This sequence represents the human tumour necrosis factor (TNF)
XX CC receptor-like 2 (TR2) protein. Antibodies that target the TR2 protein can
XX CC be used in the method of the invention to treat pathological conditions.
XX CC The method is used to treat systemic lupus erythematosus, idiopathic
XX CC thrombocytopenic purpura, rheumatoid arthritis, multiple sclerosis,
XX CC psoriasis, inflammatory bowel disease, insulin-dependent diabetes
XX CC mellitus, allergic disorders, e.g. asthma, allergic rhinitis and atopic
XX CC dermatitis, cancer, e.g. lymphomas and leukemias, atherosclerosis and
XX CC viral infections, e.g. Herpes simplex virus and AIDS. The TR2 antibody
XX CC is also used to monitor and diagnose abnormalities in TR-2 function,
XX CC production or metabolism.
XX CC
XX CC Sequence 283 AA:
SQ
XX Query Match 99.8%; Score 1575; DB 20; Length 283;
XX Best Local Similarity 99.6%; Pred. No. 2.3e-120;
XX Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPPGDMGPPPMRSTPRDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
DB 1 MEPPGDMGPPPMRSTPRDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
QY 61 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCOMCDPAMGLRASRNCSTRTENAVCG 120
DB 61 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCOMCDPAMGLRASRNCSTRTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESDTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESDTLCONCPGTFSPNGTLEECQ 180
QY 121 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCOMCDPAMGLRASRNCSTRTENAVCG 120
DB 121 YRVKEACGELTGVCPCPGTYIAHLNGLSKLCOCOMCDPAMGLRASRNCSTRTENAVCG 120
QY 181 HQTCKSMVLTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKRPBGDVVAVIYS 240
DB 181 HQTCKSMVLTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKRPBGDVVAVIYS 240
QY 241 VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
DB 241 VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
XX
XX RESULT 12
XX ID AAY94717
XX AA AAY94717 standard; Protein; 283 AA.
XX XX
```

Best Local Similarity 100.0%; Pred. No. 1.3e-120; Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMRSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVSGCCPKCSFG 60
 Db 1 MEPPGDMGPPPMRSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVSGCCPKCSFG 60
 QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCPAMGLRASRNCSTENAVCG 120
 Db 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCPAMGLRASRNCSTENAVCG 120
 QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQRVQKGTESODTLCONCPGTSPNGTLEECQ 180
 Db 121 CSPGHFCTVODGDHCAACRAVATSSPGQRVQKGTESODTLCONCPGTSPNGTLEECQ 180
 QY 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLIICVRRKPRGVDVVKYIVS 240
 Db 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLIICVRRKPRGVDVVKYIVS 240
 QY 241 VQRRQGEAGEATVIEALQAPPDVTTVAVEETIPSTFGSRPNH 283
 Db 241 VQRRQGEAGEATVIEALQAPPDVTTVAVEETIPSTFGSRPNH 283

RESULT 9
 ABU60681
 ID ABU60681 standard; Protein; 283 AA.

AC ABU60681;

DT 06-MAY-2003 (first entry)

DE Human membrane-bound Herpesvirus Entry Mediator (mHEM).

XX Human; receptor; TANGO-69 receptor; herpesvirus entry mediator; HEM;
 KW mHEM1; SHVEM2; SHVEM3; mHEM2; tumour necrosis factor receptor; TNFR;
 KW immune disorder; autoimmune disorder; arthritis; graft rejection;
 KW T-cell disorder; AIDS; inflammatory disorder; bacterial infection;
 KW psoriasis; septicemia; cerebral malaria; inflammatory bowel disease;
 KW rheumatoid arthritis; osteoarthritis; allergic inflammatory disorder;
 KW asthma; psoriasis; apoptotic disorder; rheumatoid arthritis;
 KW systemic lupus erythematosus; insulin-dependent diabetes mellitus;
 KW cytotoxic disorder; septic shock; cachexia; proliferative disorder;
 KW B-cell cancer.

OS Homo sapiens.

PN US2002132297-A1.

XX 19-SEP-2002.

PF 21-AUG-2001; 2001US-0934289.

XX 03-SEP-1998; 98US-0146950.

XX (MILL-) MILLENNIUM PHARM INC.

PI Busfield SJ;

XX WPI; 2003-246556/25.

DR N-PSDB; ABX90562.

XX New TANGO-69 receptor polynucleotides and polypeptides, useful for

PT treating arthritis, graft rejection, AIDS, bacterial infection,

PT psoriasis, septicemia, cerebral malaria, inflammatory bowel disease,

XX asthma, psoriasis, lupus

PS Disclosure; Fig 10; 79pp; English.

XX The invention relates to an isolated nucleic acid molecule, designated as

CC TANGO-69 receptor polynucleotide. TANGO-69 receptor refers to a

CC portion of the proteins SHVEM1, SHVEM2, SHVEM3 and mHEM2 (where HEM is

CC Herpesvirus Entry Mediator and "s" refers to a soluble form and "m" to a

CC membrane bound form). Also included are a host cell containing TANGO-69
 CC receptor nucleic acid, a non-human mammalian host cell containing
 CC TANGO-69 receptor nucleic acid, an isolated polypeptide that is encoded
 CC by TANGO-69 receptor nucleic acid, an antibody that selectively binds to
 CC the TANGO-69 receptor polypeptide, and identifying a compound that binds
 CC to and/or modulates the activity of the TANGO-69 receptor polypeptide.
 CC The polynucleotides, polypeptides compounds and methods are useful for
 CC treating immune disorders such as autoimmune disorders (e.g. arthritis,
 CC graft rejection), T-cell disorders (AIDS), inflammatory disorders (e.g.
 CC bacterial infection, psoriasis, septicemia, cerebral malaria,
 CC inflammatory bowel disease, rheumatoid arthritis, osteoarthritis),
 CC allergic inflammatory disorders (e.g. asthma, psoriasis),
 CC apoptotic disorders (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, insulin-dependent diabetes mellitus), cytotoxic disorders,
 CC septic shock, cachexia, and proliferative disorders (e.g. B-cell
 CC cancers). TANGO-69 receptor is a member of the TNF (tumour necrosis
 CC factor) superfamily of proteins. The present sequence represents a
 CC TANGO-69 receptor protein.

XX Sequence 283 AA;

Query Match 100.0%; Score 1578; DB 24; Length 283;

Best Local Similarity 100.0%; Pred. No. 1.3e-120; Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMRSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVSGCCPKCSFG 60
 Db 1 MEPPGDMGPPPMRSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEYVSGCCPKCSFG 60
 QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCPAMGLRASRNCSTENAVCG 120
 Db 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLCQCMCPAMGLRASRNCSTENAVCG 120
 QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQRVQKGTESODTLCONCPGTSPNGTLEECQ 180
 Db 121 CSPGHFCTVODGDHCAACRAVATSSPGQRVQKGTESODTLCONCPGTSPNGTLEECQ 180
 QY 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLIICVRRKPRGVDVVKYIVS 240
 Db 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLIICVRRKPRGVDVVKYIVS 240
 QY 241 VQRRQGEAGEATVIEALQAPPDVTTVAVEETIPSTFGSRPNH 283
 Db 241 VQRRQGEAGEATVIEALQAPPDVTTVAVEETIPSTFGSRPNH 283

RESULT 10

AAW60045
 ID AAW60045 standard; Protein; 283 AA.

XX AAW60045;

XX 25-SEP-1998 (first entry)

XX Human TNF receptor related (TR2) protein.

XX Human; tumour necrosis factor; TNF; herpes simplex virus;

KW aberrant cell survival; radiation therapy; lymphocyte proliferation;

KW immune deficiency syndrome.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..36

FT Peptide /note= "Signal peptide"

FT Peptide 37..283

FT Domain /note= "Mature peptide"

FT Modified-site 37..200

FT Modified-site /note= "Extracellular domain"

FT Modified-site /note= "Asparagine-linked glycosylation site"

FT Modified-site /note= "Asparagine-linked glycosylation site"

KM Human; tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;
 KM immune system-related disorder; inflammatory disease; immunosuppressive;
 KM bowel disease; encephalitis; atherosclerosis; gastrointestinal Gen;
 KM autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
 KM multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;
 KM graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis;
 KM neuroprotective; antiarteriosclerotic; dermatological; asthma.
 XX
 OS Homo sapiens.
 XX
 PN WO200218622-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 24-AUG-2001; 2001WO-US26396.
 XX
 PR 25-AUG-2000; 2000US-227598P.
 PR 21-NOV-2000; 2000US-252131P.
 PR 06-JUL-2001; 2001US-303224P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Gentz RL, Ebner R, Yu G, Ruben SM, Ni J, Feng P;
 XX
 DR WPI; 2002-281068/32.
 XX
 PT Novel nucleic acid molecules comprising a polynucleotide encoding human
 PT tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides
 PT useful for treating disease e.g. inflammatory and autoimmune disorders
 PT
 XX
 PS Claim 36; Page 346-347; 350pp; English.
 XX
 CC The invention relates to human tumour necrosis factor receptor (TNFR)-
 CC 6alpha and 6beta protein and their corresponding nucleic acids. The
 CC invention provides screening methods for identifying agonists and
 CC antagonists of TNFR-6alpha and 6beta activity. The invention also
 CC provides diagnostic and therapeutic methods for detecting and treating
 CC immune system-related disorders. The method is useful for treating or
 CC preventing an inflammatory disease or disorder selected from bowel
 CC disease, encephalitis, atherosclerosis and psoriasis, an autoimmune
 CC disease or disorder selected from systemic lupus erythematosus,
 CC arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
 CC and autoimmune encephalitis; graft versus host disease (GVHD), and an
 CC allergy or asthma. The present sequence is human TNFR-6alpha and TNFR-
 CC 6beta related protein.
 CC
 SQ Sequence 283 AA;
 Query Match 100.0%; Score 1578; DB 23; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1,3e-120;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 ABR40215
 ID ABR40215 standard; Protein; 283 AA.
 XX
 AC ABR40215;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human cobesin.
 XX
 KW Human; cobesin; lipid partitioning; lipid metabolism; weight reduction;
 KW insulin-like activity; free fatty acid oxidation; anorectic; antilipemic;
 KW antiarteriosclerotic; antidiabetic; hypotensive; immunomodulator;
 KW cytostatic; anti-HIV; antiinflammatory; antidepressant; weight loss;
 KW obesity.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide
 FT 1..38
 FT /label= Signal_peptide
 FT Protein
 FT 39..283
 FT /label= Mature_cobesin
 FT Domain
 FT 39..202
 FT /label= Extracellular_domain
 FT Domain
 FT 203..223
 FT /label= Transmembrane_domain
 FT Domain
 FT 224..283
 FT /label= Intracellular_domain
 XX
 PN WO2003011321-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 29-JUL-2002; 2002WO-1B03408.
 XX
 PR 31-JUL-2001; 2001US-309233P.
 XX
 PA (GSEST) GENSET SA.
 XX
 PI Lucas J, Dialynas D, Briggs K;
 XX
 DR WPI: 2003-247866/25.
 DR N-PSDB; ABZ9577.
 XX
 PT Screening for an agonist or an antagonist of cobesin activity, useful
 PT for reducing body mass, maintaining weight loss, or preventing or
 PT treating an obesity-related disease or disorder, e.g. hyperlipidemia,
 PT diabetes or hypertension
 XX
 PS Example 10; Page 34; 37pp; English.
 XX
 CC The invention relates to a novel method for screening for an agonist or
 CC an antagonist of cobesin activity, i.e. lipid partitioning, lipid
 CC metabolism, insulin-like activity, free fatty acid oxidation, or weight
 CC reduction. The method of the invention has anorectic, antilipemic,
 CC antiarteriosclerotic, antidiabetic, hypotensive, immunomodulator,
 CC cytostatic, anti-HIV, antiinflammatory, and antidepressant activity. The
 CC method is useful for screening for an agonist or antagonist of cobesin
 CC activity. The agonists or antagonists are useful for reducing body mass,
 CC maintaining weight loss, preventing or treating an obesity-related
 CC disease or disorder, e.g. hyperlipidemia, atherosclerosis, insulin
 CC resistance, diabetes or hypertension. The compounds are also useful for
 CC increasing body mass or treating disorders associated with excessive
 CC weight loss, e.g. cachexia, cancer-related weight loss, acquired
 CC immunodeficiency syndrome (AIDS)-related weight loss, chronic
 CC inflammatory disease-related weight loss or anorexia. The present
 CC sequence represents the human cobesin of the invention.
 XX
 SQ Sequence 283 AA;
 Query Match 100.0%; Score 1578; DB 24; Length 283;

QY 61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 DB 61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 QY 121 CSPGHFCIVDDGDHCAACRAVATSSPGQVQKGTSSODTLCONCPPTSPNLTLEECQ 180
 DB 121 CSPGHFCIVDDGDHCAACRAVATSSPGQVQKGTSSODTLCONCPPTSPNLTLEECQ 180
 QY 181 HQTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVIVCTVGLIICVRRKPRGQVVKYIVS 240
 DB 181 HQTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVIVCTVGLIICVRRKPRGQVVKYIVS 240
 QY 241 VQRRKQBAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
 DB 241 VQRRKQBAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
 RESULT 6
 ID AAY95348 standard; Protein; 283 AA.
 AC AAY95348;
 XX
 DT 25-SEP-2000 (first entry)
 XX
 DE Human PRO509 antitumour protein.
 XX
 KW PRO509; human; antitumour; tumour; therapy; cytostatic;
 KW breast cancer; ovarian cancer; renal cancer; colorectal cancer;
 KW uterine cancer; prostate cancer; lung cancer; bladder cancer;
 KW central nervous system cancer; melanoma; leukaemia; neoplasm.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT /label= Signal_peptide
 FT /label= 283
 FT /label= PRO509
 FT Domain
 FT /note= "transmembrane domain"
 FT 81..87
 FT /note= "N-myristoylation"
 FT 89..95
 FT /note= "N-myristoylation"
 FT 104..110
 FT /note= "N-myristoylation"
 FT 120..126
 FT /note= "N-myristoylation"
 FT 153..159
 FT /note= "N-myristoylation"
 FT 193..199
 FT /note= "N-myristoylation"
 FT 192..201
 FT /note= "N-myristoylation"
 FT 220..226
 FT /note= "N-myristoylation"
 FT 110..114
 FT /note= "Asn is N-glycosylated"
 FT 173..177
 FT /note= "Asn is N-glycosylated"
 FT 231..234
 FT /note= "cell attachment sequence"
 PN W0200037638-A2.
 XX
 XX 29-JUN-2000.
 PD
 XX
 PF 02-DEC-1999; 99WO-US28565.
 XX
 PR 22-DEC-1998; 98US-0113296.
 PR 08-MAR-1999; 99WO-US05028.
 PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;
 PI Napier MA, Pilti RM, Wood WI;
 XX
 DR WPI; 2000-442668/38.
 DR N-PSDB; AAA49727.
 XX
 PT Novel composition to inhibit neoplastic cell growth or for treating
 PT tumor in mammal comprises polypeptides PRO179, PRO207, PRO219,
 PT PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO509 or
 PT PRO866
 PS
 PS Claim 19; Fig 24; 172pp; English.
 XX
 CC The present sequence is that of human antitumour protein PRO509,
 CC as deduced from a retinal cDNA clone (see AAA49727). PRO509 shows
 CC homology to members of the human tumour necrosis factor receptor
 CC family such as the lymphotoxin-beta receptor (11 identities) and
 CC CD40 (12 identities). A claimed method for inhibiting the growth
 CC of a tumour cell comprises exposing the tumor cell to PRO179,
 CC PRO207, PRO320, PRO221, PRO224, PRO328, PRO301, PRO526,
 CC PRO362, PRO509 or PRO866 (see AAY95337-49), their agonists or
 CC chimeric polypeptides incorporating them. The tumour is especially
 CC a cancer selected from breast, ovarian, renal, colorectal, uterine,
 CC prostate, lung, bladder and central nervous system cancer, melanoma
 CC and leukaemia. Methods for the recombinant expression of the
 CC antitumour proteins are also provided.
 CC
 SQ Sequence 283 AA;
 QY
 QY 1 MEPPGDMGPPPMRSTRDTLRLVLYTFEGAPCYAPALPSCKEDEYVSGCCPKSPG 60
 DB 1 MEPPGDMGPPPMRSTRDTLRLVLYTFEGAPCYAPALPSCKEDEYVSGCCPKSPG 60
 QY 61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 DB 61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
 QY 121 CSPGHFCIVDDGDHCAACRAVATSSPGQVQKGTSSODTLCONCPPTSPNLTLEECQ 180
 DB 121 CSPGHFCIVDDGDHCAACRAVATSSPGQVQKGTSSODTLCONCPPTSPNLTLEECQ 180
 QY 181 HQTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVIVCTVGLIICVRRKPRGQVVKYIVS 240
 DB 181 HQTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVIVCTVGLIICVRRKPRGQVVKYIVS 240
 QY 241 VQRRKQBAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
 DB 241 VQRRKQBAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
 RESULT 7
 ID AAE20852 standard; Protein; 283 AA.
 AC AAE20852;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Human tumour necrosis factor receptor (TNFR) related protein.

CC treatment of arthritis or inflammation using an antibody directed against
 CC a fragment of the TR2 protein. TR2 its agonists, antagonists and
 CC antibodies exhibit cytostatic, dermatological, antianemic,
 CC immunosuppressive, antiallergic, antiarthritic, antiaesthetic,
 CC antiinflammatory, neuroprotective, nocitropic, antiparkinsonian, and
 CC cerebroprotective activity. The methods are useful for treating arthritis
 CC or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
 CC mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
 CC immunodeficiency or for enhancing an in vivo leukocyte response to an
 CC antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
 CC preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
 CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
 CC inflammatory myopathies) and immunodeficiency disorders (such as severely
 CC combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
 CC disorder, or Nezelof syndrome-combined immunodeficiency with IgA). TR2,
 CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
 CC antagonists are useful for treating or preventing autoimmune diseases and
 CC inhibit the growth, progression and/or metastasis of cancers. They are
 CC also used to activate, differentiate or proliferate cancerous cells or
 CC tissues, and can be used to treat diseases associated with increased cell
 CC survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
 CC Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
 CC as sources for generating antibodies, as molecular weight markers.
 CC This sequence represents the TR2 receptor protein of the invention.

XX Sequence 283 AA;

Query Match 100.0%; Score 1578; DB 21; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.3e-120;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDWGPWPWRSTPRITDVLRVLVLTFLGAPCAVAPALPSCKEDEYVYGSCCPKCSFG 60
 DB 1 MEPPGDWGPWPWRSTPRITDVLRVLVLTFLGAPCAVAPALPSCKEDEYVYGSCCPKCSFG 60
 QY 61 YVKEACGELTGTVCPCPPGTYYIAHLNLSKLCLOCCMDPAMGLRASNCRTEANAVG 120
 DB 61 YVKEACGELTGTVCPCPPGTYYIAHLNLSKLCLOCCMDPAMGLRASNCRTEANAVG 120
 QY 121 CSPGHFCIVQDGDHCAACRAVATSPGQVQKGTESQDTLCCNCPGTFFSPNGTLEBCQ 180
 DB 121 CSPGHFCIVQDGDHCAACRAVATSPGQVQKGTESQDTLCCNCPGTFFSPNGTLEBCQ 180
 QY 181 HQTGCSMLVTKAGAGTSSSHWMMFLSGSLVIVIVYSTGLIICVKKRRPRGDVAVIVIS 240
 DB 181 HQTGCSMLVTKAGAGTSSSHWMMFLSGSLVIVIVYSTGLIICVKKRRPRGDVAVIVIS 240
 QY 241 VORKROEAGEATVIEALCAPPDVTVAVEETIPSTGRSPNH 283
 DB 241 VORKROEAGEATVIEALCAPPDVTVAVEETIPSTGRSPNH 283

RESULT 5

AA93695
 ID AA93695 standard; protein; 283 AA.

AC AA93695;

DT 03-OCT-2000 (first entry)

DE Amino acid sequence of novel polypeptide PRO509.

XX PRO201; PRO292; PRO327; PRO1265; PRO344; PRO347; PRO357;
 XX PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
 XX tumorigenesis; cancer; neoplastic cell growth; cell proliferation.

OS Homo sapiens.

XX Key location/Qualifiers

FT Peptide 1..36

FT Modified-site /note= "signal sequence"

FT /note= "N-myristoylation site"

FT Modified-site 89..95
 FT /note= "N-myristoylation site"
 FT Modified-site 104..110
 FT /note= "N-myristoylation site"
 FT Modified-site 110..114
 FT /note= "N-glycosylation site"
 FT Modified-site 120..126
 FT /note= "N-myristoylation site"
 FT Modified-site 153..159
 FT /note= "N-myristoylation site"
 FT Modified-site 173..177
 FT /note= "N-glycosylation site"
 FT Modified-site 193..199
 FT /note= "N-myristoylation site"
 FT Modified-site 195..201
 FT /note= "N-myristoylation site"
 FT Domain 203..222
 FT /note= "transmembrane domain"
 FT Modified-site 220..226
 FT /note= "N-myristoylation site"
 FT Region 231..234
 FT /note= "cell attachment sequence"

XX WO200037640-A2.

XX 29-JUN-2000.

XX 16-DEC-1999; 99WO-US30095.

XX 22-DEC-1998; 98US-011296.

XX 08-MAR-1999; 99WO-US05028.

XX 02-JUN-1999; 99WO-US12252.

XX 01-SEP-1998; 99WO-US20111.

XX 15-SEP-1998; 99WO-US21090.

XX 30-NOV-1999; 99WO-US28313.

XX 30-NOV-1999; 99WO-US28409.

XX 01-DEC-1999; 99WO-US28301.

XX 02-DEC-1999; 99WO-US28565.

XX (GENTH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
 XX Wood WJ;
 XX WPI: 2000-452188/39.
 XX N-PSDB; AAA46931.

XX New anti-polypeptide antibody useful in the treatment and diagnosis of
 XX neoplastic cell growth and proliferation -
 XX Claim 61; Fig 24; 220pp; English.

XX The present sequence represents a novel human polypeptide. The
 XX specification describes novel polypeptides designated PRO201, PRO292,
 XX PRO327, PRO1265, PRO343, PRO347, PRO357, PRO715, PRO1017,
 XX PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in
 XX the genome of tumour cells. The polypeptides are believed to contribute
 XX to tumorigenesis. The polypeptides are useful target for the
 XX identification of certain cancers, and may act as predictors of the
 XX prognosis of tumour treatment. Antibodies against these polypeptides
 XX are useful in the treatment and diagnosis of neoplastic cell growth
 XX and proliferation in mammals.

XX Sequence 283 AA;

Query Match 100.0%; Score 1578; DB 21; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.3e-120;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDWGPWPWRSTPRITDVLRVLVLTFLGAPCAVAPALPSCKEDEYVYGSCCPKCSFG 60
 DB 1 MEPPGDWGPWPWRSTPRITDVLRVLVLTFLGAPCAVAPALPSCKEDEYVYGSCCPKCSFG 60

```

RESULT 3
AA06488
ID AA06488 standard; Protein; 283 AA.
XX
XX AC AA06488;
XX
XX DT 27-SEP-1999 (first entry)
XX
XX DE Human tumour-associated protein PRO509.
XX
XX KW PRO1112; UNQ555; cancer; tumour necrosis factor receptor;
XX diagnosis; therapy; human.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 201..225
FT /note="transmembrane domain"
FT 226..283
FT /note="cytoplasmic domain"
FT
XX WO9935170-A2.
XX
XX 15-JUL-1999.
XX
XX 05-JAN-1999; 99WO-US00106.
XX
XX 20-NOV-1998; 98US-0109304.
XX 05-JAN-1998; 98US-0070440.
XX 29-APR-1998; 98US-0083500.
XX 22-MAY-1998; 98US-0086414.
XX 10-JUN-1998; 98US-0088742.
XX 10-NOV-1998; 98US-0107783.
XX
XX (GETH ) GENENTECH INC.
XX
XX Boetstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
XX Roy MA, Wood WT;
XX
XX WPI; 1999-430385/36.
XX DR N-PSDB; AAX87265.
XX
XX Antibody against proteins expressed in neoplastic cells, useful for
XX tumor diagnosis and treatment
XX
XX Example 1; Fig 24; 162pp; English.
XX
XX This sequence represents human PRO509 (UNQ329), a protein encoded
XX by the novel cDNA clone DNA50148 (see AAX87264), and a member of the
XX tumour necrosis factor receptor family. Amplification of DNA50148
XX was observed in various tumour tissues, suggesting a role in tumour
XX formation or growth. Antagonists (e.g. antibodies) directed to
XX PRO509 may have use in cancer therapy. The invention identifies
XX 14 genes (see AAX87264-67) that are amplified in the genome of tumour
XX cells. Such amplification is expected to be associated with
XX overexpression of the gene product and to contribute to tumorigenesis.
XX The encoded proteins (see AA06477-90) may be useful targets for the
XX diagnosis and/or treatment (including prevention) of certain cancers,
XX and may act as predictors of the prognosis of tumour treatment.
XX Antibodies that bind the proteins are claimed and used in claimed
XX cancer diagnostic kits.
XX
XX Sequence 283 AA:
XX
Query Match 100.0%; Score 1578; DB 20; Length 283;
Best Local Similarity 100.0%; Pred. No. 1,3e-120;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEPPDMDGPPRRSRPTDVLRLVYLFLGAPCYAAPLPSCXENDEYVGSCECPKSPG 60
1 MEPPDMDGPPRRSRPTDVLRLVYLFLGAPCYAAPLPSCXENDEYVGSCECPKSPG 60

```

QY	61	RRVKACCELIGTVEPCPGTYIAHLNGLISKLCQCOMCDPAMGLRASNCSTENAVCG	120
DB	61	YRVKACCELIGTVEPCPGTYIAHLNGLISKLCQCOMCDPAMGLRASNCSTENAVCG	120
QY	121	CSPGHFCIVDDGDHCAACRAVATSSPGORVQKGTESODTLQNCPCPGTSPNGTLEECQ	180
DB	121	CSPGHFCIVDDGDHCAACRAVATSSPGORVQKGTESODTLQNCPCPGTSPNGTLEECQ	180
QY	181	HOTKCSMLVTAGAGTSSSHWWMLSSGLVIVVICSITVGLIICVKKRRPRGDVAVVVS	240
DB	181	HOTKCSMLVTAGAGTSSSHWWMLSSGLVIVVICSITVGLIICVKKRRPRGDVAVVVS	240
QY	241	VQRKQBAEGEATVIEALQAPPDVTVVAEETIPFTGRSPNH	283
DB	241	VQRKQBAEGEATVIEALQAPPDVTVVAEETIPFTGRSPNH	283
RESULT 4			
AAV94721			
ID	AAV94721	standard; Protein; 283 AA.	
AC	AAV94721;		
XX			
DT	29-JAN-2001	(first entry)	
XX			
DE		Human TR2-receptor protein sequence.	
XX			
KM		Tumour necrosis factor-receptor related protein; TR2; human; cancer;	
KW		chromosome p16.2-p16.3; arthritis; inflammation; autoimmune disease;	
KW		immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;	
KM		severely combined immunodeficiency; apoptosis inhibition;	
KW		Alzheimer's disease; Parkinson's disease; Crohn's disease.	
XX			
OS		Homo sapiens.	
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..38	
FT	Protein	/note= "Signal peptide"	
FT		39..283	
FT		/label= "TR2 receptor"	
XX			
PN	WO200056405-A2.		
XX			
PD	28-SEP-2000.		
XX			
PF	22-MAR-2000; 2000WO-US07521.		
XX			
PR	22-MAR-1999; 99US-0125683.		
PR	26-MAR-1999; 99US-0126522.		
PR	20-MAY-1999; 99US-0135169.		
PR	06-AUG-1999; 99US-0147383.		
XX			
PA	(NIJ/) NI J.		
PA	(ROSE/) ROSEN C A.		
XX	(GENT/) GENTZ R L.		
PI	NI J, Rosen CA, Gentz RL;		
XX			
DR	WPI: 2000-594519/56.		
DR	N-PSDB: AAA28149.		
XX			
PT		Nucleic acid molecule encoding a human tumor necrosis factor receptor 2	
PT		and its splice variants, useful for treating arthritis or	
PT		inflammation, cancer (such as follicular lymphomas) and	
PT		immunodeficiency disorders -	
XX			
PS	Disclosure; Page 370; 373pp; English.		
CC		This invention relates to an isolated nucleic acid molecule encoding a	
CC		human tumor necrosis factor (TNF)-receptor related protein TR2. Included	
CC		in the invention are the two splice variants of TR2, TR2-Sv1 and TR2-Sv2.	
CC		The TR2 gene is located on chromosome 1 at position p16.2-p16.3. TR2 is a	
CC		member of the TNFR superfamily. The invention includes a method for the	

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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:26:45 ; Search time 40 Seconds

(without alignments)
1122.991 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578

Sequence: 1 MEPPGDWGPFPWRSTPRTDV.....VTVAVEETIDPSFTGRSPNH 283

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1578	100.0	283	AAW05809	Human tumour necro
2	1578	100.0	283	AAW69238	Herpesvirus entry
3	1578	100.0	283	AAW06488	Human tumour-asso
4	1578	100.0	283	AAW94721	Human TR2-receptor
5	1578	100.0	283	AAW93695	Amino acid sequenc
6	1578	100.0	283	AAW95348	Human PRO509 antit
7	1578	100.0	283	AAW20852	Human tumour necro
8	1578	100.0	283	ABR40215	Human cohesin. Ho
9	1578	100.0	283	ABU60681	Human membrane-bou

10	1575	99.8	283	AAW60045	Human TNF receptor
11	1575	99.8	283	AAW87591	Human tumour necro
12	1575	99.8	283	AAW94717	Human TR2-receptor
13	1572	99.6	283	AAW65031	Tumour necrosis fa
14	1570	99.5	283	AAW12659	Human herpes simpi
15	1570	99.5	283	AAW05797	Herpes virus entry
16	1373.5	87.0	277	AAW79207	Membrane-bound her
17	1373.5	87.0	277	AAW06694	Human membrane-bou
18	1152.5	73.0	239	ABU60695	Human mature membr
19	1068	67.7	193	AAW79204	Soluble herpesvtru
20	1068	67.7	193	ABU60675	Human soluble Herp
21	1060	67.2	197	AAW79205	Soluble herpesvtru
22	1060	67.2	197	ABU60682	Human soluble Herp
23	1058	67.0	186	AAW79206	Soluble herpesvtru
24	1058	67.0	186	ABU60688	Human soluble Herp
25	847	53.7	155	ABU60676	Human mature solub
26	843	53.4	148	ABU60689	Human mature solub
27	839	53.2	159	ABU60683	Human mature solub
28	604.5	38.3	185	AAW60046	Human TNF receptor
29	604.5	38.3	185	AAW94716	Human TR2-receptor
30	604.5	38.3	240	AAW05810	Human tumour necro
31	393	24.9	136	AAW60047	Human TNF receptor
32	393	24.9	136	AAW94719	Human TR2-receptor
33	377.5	23.9	134	AAW05811	Human tumour necro
34	332	21.0	278	AAW95322	Pig costimulatory
35	276.5	17.5	281	AAW94715	Murine CD40 protei
36	268.5	17.0	277	AAW32191	CD40 protein. Uni
37	267.5	17.0	276	AAW33499	Human CD40 protein
38	267.5	17.0	277	AAW38859	CD40 protein. Hom
39	267.5	17.0	277	AAW52701	Human CD40 protein
40	267.5	17.0	277	AAW84892	Human CD40 antigen
41	267.5	17.0	277	AAW50520	Human tumour necro
42	267.5	17.0	277	AAW37807	Human CD40. Homo
43	267.5	17.0	277	AAW018051	CD40 B-cell antige
44	267.5	17.0	277	AAW19354	Human CD40 antigen
45	267.5	17.0	277	ABR40010	Human Moxifin. Ho

ALIGNMENTS

RESULT 1	
AAW05809	
ID	AAW05809 standard; Protein; 283 AA.
XX	
AC	AAW05809;
XX	
DT	30-JUN-1997 (first entry)
XX	
DE	Human tumour necrosis factor receptor.
XX	
KW	Human, tumour necrosis factor; TNF; receptor; treatment;
KW	activation; inhibition; identification; agonist; antagonist;
KW	stimulation; T cell; differentiation; mediation; immune;
KW	antiviral; response; regulation; growth; protection; HIV;
KW	radiation; Chlamydia; infection; immunodeficiency; virus;
KW	autoimmune disease; inflammation; septic shock; cerebral;
KW	cachexia; B cell; cancer; graft; host; reaction; rejection;
KW	prevention; apoptosis; cytotoxicity; hybridisation probe;
KW	detection; antibody; reagent.
XX	
OS	Homo sapiens.
XX	
FH	
FT	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..38
FT	/label= sig_peptide
FT	39..283
FT	Peptide
XX	/label= mat_peptide
XX	
PN	WO9634095-A1.
XX	
XX	
PD	31-OCT-1996.
XX	

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-27

Query Match 17.0%; Score 267.5; DB 3; Length 276;
Best Local Similarity 26.1%; Pred. No. 2,1e-16;
Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

QY 20 VRLVLYLFLGAPCYAPAL-----PSCKEDEVPGSECCPKSPGYRVKACGELTGV 74
DB 1 MVRLLPQCVMWG--CLLTAVHPEPPTACREKQYLINSQCCLQPGQKLVSDETFETE 58
QY 75 CERCPRGTYIAHNGSKLQCCMCDBPAGLRASRNCSTENAVGCGSPGHFCIVQDDGH 134
DB 59 CLPGESEFLDTWNRETHCHQHKYCDPNLGLRVQKGTSETPTICTCEBGMHC--TSEA 115
QY 135 CAACRAVATSSPGQAVQKGTESQDTLCONCPGTFPS--PNGTLEBECOHQTKCSW--LVTK 191
DB 116 CESCVAHRSCSPGFGVKQATAGSDTICBPCPVGFSNVSAFEKCHPWTSCETKDLVQ 175
QY 192 AAGTSSSHVMWFLSGSLVIVVCSVGILICVKKRRKRGDVVKVIVSVQRRQDEAGE 251
DB 176 Q-AGTKTIDVCGPQDRALALVPIPIFGILFA-----ILLVIVFIKKVAKKPTNK 225
QY 252 ATVIELQAPPDV-----TTAVRETI 273
DB 226 AP--HPKQEPQETINPPDDLPGSNTAAPVOETL 255

Search completed: November 14, 2003, 17:32:51
Job time : 22 secs

US-09-146-950-20
; Sequence 20, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-20

Query Match 53.2%; Score 839; DB 3; Length 159;
Best Local Similarity 98.0%; Pred. No. 4,8e-68;
Matches 146; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 39 LPSCDEDPYVSGECPCPKSPGYRKEACGELTGTVCPCPPGTYYIAHLNGLSKLQCOM 98
DB 1 LPSCDEDPYVSGECPCPKSPGYRKEACGELTGTVCPCPPGTYYIAHLNGLSKLQCOM 60
QY 99 CDPAMGLRASRNCSTENAVCGSPGHFCIVODGDHCAACRAVATSSPGORVOKGTSQ 158
DB 61 CDPAMGLRASRNCSTENAVCGSPGHFCIVODGDHCAACRAVATSSPGORVOKGTSQ 120
QY 159 DTLQNCPPGTSPNGTLEBQCHOTKCSW 187
DB 121 DTLQNCPPGTSPNGTLEBQCHOTKCSW 147

RESULT 13
US-09-146-950-25
; Sequence 25, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-25

Query Match 23.1%; Score 365; DB 3; Length 77;
Best Local Similarity 95.5%; Pred. No. 7,7e-26;
Matches 64; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 121 CSPGHFCTVODGDHCAACRAVATSSPGORVOKGTSQDTLQNCPPGTSPNGTLEBQ 180
DB 1 CSPGHFCTVODGDHCAACRAVATSSPGORVOKGTSQDTLQNCPPGTSPNGTLEBQ 60
QY 181 HOTKCSW 187
DB 61 HOT--NW 65

RESULT 14
US-09-042-785A-11
; Sequence 11, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
US-09-042-785A-11

TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
; NAME: Mandagouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-11

Query Match 17.5%; Score 276.5; DB 3; Length 289;
Best Local Similarity 27.9%; Pred. No. 3,4e-17;
Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;

QY 41 SCKDEDPYVSGECPCPKSPGYRKEACGELTGTVCPCPPGTYYIAHLNGLSKLQCOM 100
DB 25 TCSDKQYLHGGQCCDLQPPSRRLSHHTALEKTQCHPCDSGERSAQNRRIRCHQHNC 84
QY 101 PAMGLRASRNCSTENAVCGSPGHFCIVODGDHCAACRAVATSSPGORVOKGTSQDT 160
DB 85 PNOGLRYKKEGTAEEDTCTCKEGHCTSKD--CEACAQHTPCIPGFGVEMATETTTDT 141
QY 161 LQNCPPGTSPNGTLEBQCHOTKCS---WLVTAGACTSSSHWVWFLSGSLVIVY 215
DB 142 VCHPCPVGFSPNOSLSLEKCYPWTSCBDKNLEVLQK--GTSQTNVYCGLSKMRALVI 198
QY 216 CSTVGLIIC-----VKR--RKPRGDVVIVSVORKEAGEATVIALQAPPDVT 266
DB 199 PVVMGILITTFGVFLVKKVKKPXN--EMLPPAARQDPQWME-----DYPGHNTA 249
QY 267 VAVBETI 273
DB 250 APVQETL 256

RESULT 15
US-09-041-886-27
; Sequence 27, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabinzaden, Sharrow
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:

NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-09-631-780-7

Query Match 68.0%; Score 1073; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
DB 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
QY 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEBQ 180
QY 181 HOTKC 185
DB 181 HOTKC 185

RESULT 9
US-09-146-950-2
Sequence 2, Application US/09146950A
Patent No. 6287808

GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-2

Query Match 67.7%; Score 1068; DB 3; Length 193;
Best Local Similarity 98.4%; Pred. No. 1.6e-88;
Matches 184; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
DB 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
QY 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEBQ 180
QY 181 HOTKCSW 187
DB 181 HOTKCSW 187

RESULT 10
US-09-146-950-18
Sequence 18, Application US/09146950A
Patent No. 6287808

GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 197
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-18

Query Match 67.2%; Score 1060; DB 3; Length 197;
Best Local Similarity 98.4%; Pred. No. 8.6e-88;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
DB 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTFGLAPCYAPALPSCKEDEYPVGSCECPKCSFG 60
QY 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCMCDPMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLCONCPGTFSPNGTLEBQ 180
QY 181 HOTKCSW 187
DB 181 HOT -NW 185

RESULT 11
US-09-146-950-4
Sequence 4, Application US/09146950A
Patent No. 6287808

GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 155
TYPE: PRT
ORGANISM: Homo sapiens
US-09-146-950-4

Query Match 53.7%; Score 847; DB 3; Length 155;
Best Local Similarity 98.0%; Pred. No. 8.8e-69;
Matches 146; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 39 LPSCKEDEYPVGSCECPKCSFGYVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCM 98
DB 1 LPSCKEDEYPVGSCECPKCSFGYVKEACGELTGTCVCEPCPGTYIAHLNGLSKLCQCM 98
QY 99 CDPAMGLRASRNCSTENAVCGCSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQ 158
DB 61 CDPAMGLRASRNCSTENAVCGCSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQ 120
QY 159 DTLCONCPGTFSPNGTLEBQHOTKCSW 187
DB 121 DTLCONCPGTFSPNGTLEBQHOTKCSW 149

RESULT 12

STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12374
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Northrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: NOR3446P020PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
TELEFAX: (312) 616-5460
TELEX: --
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12374-2

Query Match 99.5%; Score 1570; DB 5; Length 283;
Best Local Similarity 99.3%; Pred. No. 2e-133;
Matches 281; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECCPKCSPG 60
DB 1 MEPPGDMGPPPMSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECCPKCSPG 60
QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGTFSPNGTLEECQ 180
QY 181 HQTCSMLVTKAGAGTSSSHWMMFLSGSLVIVVCSVGLIICVKKRKRGGDVVKYIVS 240
DB 181 HQTCSMLVTKAGAGTSSSHWMMFLSGSLVIVVCSVGLIICVKKRKRGGDVVKYIVS 240
QY 241 VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTFGSRPNH 283
DB 241 VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTFGSRPNH 283

RESULT 6
US-08-509-024-7

; Sequence 7, Application US/08509024B
; Patent No. 6291207
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: MONTGOMERY, Rebecca I.
; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
; FILE REFERENCE: 0290-1
; CURRENT APPLICATION NUMBER: US/08/509,024B
; CURRENT FILING DATE: 1995-07-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-509-024-7

Query Match 68.0%; Score 1073; DB 3; Length 419;

Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECCPKCSPG 60
DB 1 MEPPGDMGPPPMSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECCPKCSPG 60
QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGTFSPNGTLEECQ 180
QY 181 HQTCC 185
DB 181 HQTCC 185

RESULT 7
US-09-333-279-7

; Sequence 7, Application US/09333279
; Patent No. 630336
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: MONTGOMERY, Rebecca I.
; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
; FILE REFERENCE: 0290-1
; CURRENT APPLICATION NUMBER: US/09/333,279
; CURRENT FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-333-279-7

Query Match 68.0%; Score 1073; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECCPKCSPG 60
DB 1 MEPPGDMGPPPMSTRTDVLRLVLTFLGAPCYAPALPSCKEDEYPVGSCECCPKCSPG 60
QY 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCEPCPGTYIAHLNGLSKLQCMCDPAMGLASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQRYQKGTESQDTLCONCPGTFSPNGTLEECQ 180
QY 181 HQTCC 185
DB 181 HQTCC 185

RESULT 8
US-09-631-780-7

; Sequence 7, Application US/09631780
; Patent No. 6573058
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: MONTGOMERY, Rebecca I.
; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
; FILE REFERENCE: 0290-1
; CURRENT APPLICATION NUMBER: US/09/631,780
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US/08/509,024B
; PRIOR FILING DATE: 1995-07-25

APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/333,279
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-333-279-2

Query Match 100.0%; Score 1578; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.8e-134;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMWRSTRTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVGSECCPKCSFG 60
DB 1 MEPPGDMGPPMWRSTRTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVGSECCPKCSFG 60
QY 61 YRVEKACGELTGVCPCPGTYIAHLNGLSKLQCCMDPAMGLPASNCRSTENAVCG 120
DB 61 YRVEKACGELTGVCPCPGTYIAHLNGLSKLQCCMDPAMGLPASNCRSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTGLIICVRRKPRGDVAVIYS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTGLIICVRRKPRGDVAVIYS 240
QY 241 VORRQOAEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283
DB 241 VORRQOAEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283

RESULT 3
US-09-631-780-2
Sequence 2, Application US/09631780
Patent No. 6573058
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/631,780
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US/08/509,024B
PRIOR FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-631-780-2

Query Match 100.0%; Score 1578; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.8e-134;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMWRSTRTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVGSECCPKCSFG 60
DB 1 MEPPGDMGPPMWRSTRTDVLRLVLYLFLGAPCYAPALPSCKEDEYPVGSECCPKCSFG 60
QY 61 YRVEKACGELTGVCPCPGTYIAHLNGLSKLQCCMDPAMGLPASNCRSTENAVCG 120
DB 61 YRVEKACGELTGVCPCPGTYIAHLNGLSKLQCCMDPAMGLPASNCRSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEECQ 180

DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTGLIICVRRKPRGDVAVIYS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTGLIICVRRKPRGDVAVIYS 240
QY 241 VORRQOAEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283
DB 241 VORRQOAEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283

RESULT 4
US-09-072-993C-2
Sequence 2, Application US/09072993C
Patent No. 6346388
GENERAL INFORMATION:
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
FILE REFERENCE: GH-50030
CURRENT APPLICATION NUMBER: US/09/072,993C
CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/056,980
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/057,550
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-072-993C-2

Query Match 99.6%; Score 1572; DB 4; Length 283;
Best Local Similarity 99.6%; Pred. No. 1.3e-133;
Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 YRVEKACGELTGVCPCPGTYIAHLNGLSKLQCCMDPAMGLPASNCRSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTGLIICVRRKPRGDVAVIYS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWMFLSGSLVIVICSTGLIICVRRKPRGDVAVIYS 240
QY 241 VORRQOAEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283
DB 241 VORRQOAEAGEATVIEALQAPPDVTVAVEETIPSTGSPNH 283

RESULT 5
PCT-US96-12374-2
Sequence 2, Application PC/TUS9612374
GENERAL INFORMATION:
APPLICANT: Northwestern University
TITLE OF INVENTION: Herpes Virus Entry Mediator
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, Suite 4700
CITY: Chicago

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2003, 17:29:30 ; Search time 21 Seconds
(without alignments)
570.189 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578
Sequence: 1 MEPPGDMGPPWRSTPRDV.....VTVAVEETIPSTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1578	100.0	283	3	US-08-509-024-2
2	1578	100.0	283	4	US-09-333-279-2
3	1578	100.0	283	4	US-09-631-780-2
4	1572	99.6	283	4	US-09-072-993C-2
5	1570	99.5	283	5	PCT-US96-12374-2
6	1073	68.0	419	3	US-08-509-024-7
7	1073	68.0	419	4	US-09-333-279-7
8	1073	68.0	419	4	US-09-631-780-7
9	1068	67.7	193	4	US-09-146-950-2
10	1060	67.2	193	3	US-09-146-950-18
11	847	53.7	155	3	US-09-146-950-4
12	839	53.2	159	3	US-09-146-950-20
13	365	23.1	77	3	US-09-146-950-25
14	276.5	17.5	289	3	US-09-042-785A-11
15	267.5	17.0	276	3	US-09-041-886-27
16	267.5	17.0	277	3	US-09-042-785A-10
17	267.5	17.0	277	3	US-09-006-353A-10
18	267.5	17.0	277	4	US-08-114-944D-2
19	267.5	17.0	277	4	US-09-573-986-10
20	267.5	17.0	277	4	US-08-338-975A-2
21	260	16.5	207	3	US-08-974-022-47
22	260	16.5	207	3	US-08-795-445A-47
23	260	16.5	207	3	US-08-795-447A-47
24	260	16.5	207	3	US-08-974-186-47
25	260	16.5	207	3	US-08-795-446B-47
26	260	16.5	207	4	US-08-706-945D-133
27	260	16.5	325	1	US-08-292-549-2

28	260	16.5	325	3	US-09-042-785A-9	Sequence 9, Appli
29	260	16.5	325	5	PCT-US91-02207-2	Sequence 2, Appli
30	259	16.4	45	3	US-09-146-950-9	Sequence 9, Appli
31	259	16.4	227	3	US-08-974-022-48	Sequence 48, Appli
32	259	16.4	227	3	US-08-795-445A-48	Sequence 48, Appli
33	259	16.4	227	3	US-08-795-447A-48	Sequence 48, Appli
34	259	16.4	227	3	US-08-974-186-48	Sequence 48, Appli
35	259	16.4	227	3	US-08-795-446B-48	Sequence 48, Appli
36	259	16.4	227	4	US-08-706-945D-134	Sequence 134, App
37	259	16.4	235	4	US-09-326-194-4	Sequence 4, Appli
38	259	16.4	235	4	US-09-580-235-4	Sequence 4, Appli
39	259	16.4	235	4	US-09-580-235-8	Sequence 8, Appli
40	259	16.4	235	4	US-09-580-181-4	Sequence 4, Appli
41	259	16.4	235	4	US-09-580-181-8	Sequence 8, Appli
42	259	16.4	235	4	US-09-102-530-4	Sequence 4, Appli
43	259	16.4	235	4	US-09-102-530-8	Sequence 8, Appli
44	259	16.4	257	4	US-09-579-845-10	Sequence 10, Appli
45	259	16.4	461	1	US-08-385-229-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-08-509-024-2
; Sequence 2, Application US/08509024B
; Parent No. 6291207
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
; FILE REFERENCE: 0290-1
; CURRENT APPLICATION NUMBER: US/08/509,024B
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-509-024-2

Query Match      100.0%; Score 1578; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 3 8e-134;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPWRSTPRDVRLVLYLTFLGAPCYAPALPSCKEDYPVGSCECPKSPG 60
DB 1 MEPPGDMGPPWRSTPRDVRLVLYLTFLGAPCYAPALPSCKEDYPVGSCECPKSPG 60
QY 61 YRVEACGELTGTCCEPCPGTYIAHNGLSKLCQCMCPAMGLRASRNCSTENAVCG 120
DB 61 YRVEACGELTGTCCEPCPGTYIAHNGLSKLCQCMCPAMGLRASRNCSTENAVCG 120
QY 121 CSPHFCIVDDGDHCAACRAVATSSPGORVOKGTEBODFLACNCPGTGFPNGTLEECQ 180
DB 121 CSPHFCIVDDGDHCAACRAVATSSPGORVOKGTEBODFLACNCPGTGFPNGTLEECQ 180
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DB 241 VORRQGEAEGBATVIEALQAPPDVTVVAVEETIPSTGRSPNH 283

--RESULT 2
US-09-333-279-2
; Sequence 2, Application US/09333279
; Parent No. 630336
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:30:26 ; Search time 175 Seconds

(without alignment)
1471.469 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578

Sequence: 1 MEPPGDWGPWPWRSTPRDV.....VTYVAVEETIPSTGRSPNH 283

Scoring table: BLOSUM62

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match
Maximum Match
Listing first

Database : Pending Patent
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32: /cgn2_6/ptc

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	1578	100.0	283	1 PCT-US01-26396-31 Sequence 31, Appl

2	1578	100.0	283	1 PCT-US02-29560-288	Sequence 288, App
3	1578	100.0	283	1 PCT-US03-10956-48	Sequence 48, Appl
4	1578	100.0	283	1 PCT-US95-05058-2	Sequence 2, Appl
5	1578	100.0	283	1 PCT-US99-20180-13	Sequence 13, Appl
6	1578	100.0	283	8 US-08-462-315-2	Sequence 2, Appl
7	1578	100.0	283	8 US-08-462-315-2	Sequence 2, Appl
8	1578	100.0	283	8 US-08-462-315-2	Sequence 2, Appl
9	1578	100.0	283	11 US-08-741-095B-26	Sequence 26, Appl
10	1578	100.0	283	13 US-08-987-902-1	Sequence 1, Appl
11	1578	100.0	283	17 US-09-342-767-13	Sequence 13, Appl
12	1578	100.0	283	18 US-09-480-284-1	Sequence 1, Appl
13	1578	100.0	283	19 US-09-533-262-26	Sequence 26, Appl
14	1578	100.0	283	22 US-09-791-537-41397	Sequence 41397, A
15	1578	100.0	283	23 US-09-882-636-46	Sequence 46, Appl
16	1578	100.0	283	23 US-09-886-342-60	Sequence 60, Appl
17	1578	100.0	283	24 US-09-924-231-2	Sequence 2, Appl
18	1578	100.0	283	24 US-09-934-289A-13	Sequence 13, Appl
19	1578	100.0	283	24 US-09-935-727-31	Sequence 31, Appl
20	1578	100.0	283	28 US-10-245-882-288	Sequence 288, App
21	1578	100.0	283	29 US-10-369-300-2	Sequence 2, Appl
22	1578	100.0	283	30 US-10-410-308-42	Sequence 42, Appl
23	1578	100.0	283	30 US-10-418-242-31	Sequence 31, Appl
24	1578	100.0	283	32 US-10-418-242-31	Sequence 32, Appl

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Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rpm and .rpm

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapm

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

RESULT 1
PCT-US01-26396-31
Sequence 31, Application PC/TUS0126396
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: P454PC73
CURRENT APPLICATION NUMBER: PCT/US01/26396
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-26396-31
Query Match 100.0%; Score 1578; DB 1; Length 283;

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Best Local Similarity 100.0%; Pred. No. 7.2e-119; Indels 0; Gaps 0;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 CSPGFCIVQGDHCAACRAVATSSPGQVKGSTESODTLCCNCPPTFSFNGTLESCQ 180
QY 181 HOTKSMVLTKAGAGTSSSHVWVWFLSGSLVIVICSTVGLICVKRRKPGDVVKYIVS 240
DB 181 HOTKSMVLTKAGAGTSSSHVWVWFLSGSLVIVICSTVGLICVKRRKPGDVVKYIVS 240
QY 241 VÖRRÖBAGBAGATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
DB 241 VÖRRÖBAGBAGATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283

RESULT 2

PCT-US02-29560-288
; Sequence 288, Application PC/TUS0229560
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-002710PC
; CURRENT APPLICATION NUMBER: PCT/US02/29560
; PRIOR FILING DATE: 2025-11-01
; PRIOR APPLICATION NUMBER: US 60/323,469
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 288
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560-288

Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119; Indels 0; Gaps 0;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPGDMPPPMRSTPRDVLRLVLYLFLGAPCAPALPSCKEDEYVSGECPCPKSPG 60
DB 1 MPPGDMPPPMRSTPRDVLRLVLYLFLGAPCAPALPSCKEDEYVSGECPCPKSPG 60
QY 61 YRVKACGELTGVCPCPGTYIAHLNGLSKLCQCCDPMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGVCPCPGTYIAHLNGLSKLCQCCDPMGLRASRNCSTENAVCG 120
QY 121 CSPGFCIVQGDHCAACRAVATSSPGQVKGSTESODTLCCNCPPTFSFNGTLESCQ 180
DB 121 CSPGFCIVQGDHCAACRAVATSSPGQVKGSTESODTLCCNCPPTFSFNGTLESCQ 180
QY 181 HOTKSMVLTKAGAGTSSSHVWVWFLSGSLVIVICSTVGLICVKRRKPGDVVKYIVS 240
DB 181 HOTKSMVLTKAGAGTSSSHVWVWFLSGSLVIVICSTVGLICVKRRKPGDVVKYIVS 240
QY 241 VÖRRÖBAGBAGATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
DB 241 VÖRRÖBAGBAGATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283

DB 241 VÖRRÖBAGBAGATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283

RESULT 3

PCT-US03-10956-48
; Sequence 48, Application PC/TUS0310956
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Specifically Bind to T15
; FILE REFERENCE: PF581PCT
; CURRENT APPLICATION NUMBER: PCT/US03/10956
; PRIOR FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 60/372,087
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-10956-48

Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119; Indels 0; Gaps 0;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPGDMPPPMRSTPRDVLRLVLYLFLGAPCAPALPSCKEDEYVSGECPCPKSPG 60
DB 1 MPPGDMPPPMRSTPRDVLRLVLYLFLGAPCAPALPSCKEDEYVSGECPCPKSPG 60
QY 61 YRVKACGELTGVCPCPGTYIAHLNGLSKLCQCCDPMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGVCPCPGTYIAHLNGLSKLCQCCDPMGLRASRNCSTENAVCG 120
QY 121 CSPGFCIVQGDHCAACRAVATSSPGQVKGSTESODTLCCNCPPTFSFNGTLESCQ 180
DB 121 CSPGFCIVQGDHCAACRAVATSSPGQVKGSTESODTLCCNCPPTFSFNGTLESCQ 180
QY 181 HOTKSMVLTKAGAGTSSSHVWVWFLSGSLVIVICSTVGLICVKRRKPGDVVKYIVS 240
DB 181 HOTKSMVLTKAGAGTSSSHVWVWFLSGSLVIVICSTVGLICVKRRKPGDVVKYIVS 240
QY 241 VÖRRÖBAGBAGATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
DB 241 VÖRRÖBAGBAGATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283

RESULT 4

PCT-US95-05058-2
; Sequence 2, Application PC/TUS9505058
; GENERAL INFORMATION:
; APPLICANT: NI, ET AL.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESS: CROCHT, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05058
; FILING DATE: Concurrently
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-255
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-05058-2

Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 7,2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSPTRTDVLRLVLYLFTLGPAYAPALPSCKEDEYPVGSECCPKCSPG 60
DB 1 MEPPGDMGPPMRSPTRTDVLRLVLYLFTLGPAYAPALPSCKEDEYPVGSECCPKCSPG 60
QY 61 YRVKACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTIYODGDHCAACRAVATSSPGQRYQKGTESQDTLQNCNCPGTSPNGTLEECQ 180
DB 121 CSPGHFCTIYODGDHCAACRAVATSSPGQRYQKGTESQDTLQNCNCPGTSPNGTLEECQ 180
QY 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKRKRGVVKVIYS 240
DB 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKRKRGVVKVIYS 240
QY 241 VQRKROAEAGETATVIALQAPDVTVAVEETIPSTGSPNH 283
DB 241 VQRKROAEAGETATVIALQAPDVTVAVEETIPSTGSPNH 283

RESULT 5
PCT-US99-20180-13
Sequence 13, Application PC/TUS9920180
GENERAL INFORMATION:
APPLICANT: Millennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
FILE REFERENCE: 09404/079M01
CURRENT APPLICATION NUMBER: PCT/US99/20180
EARLIER FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: US 09/342,767
EARLIER FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
PCT-US99-20180-13

Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 7,2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPPGDMGPPMRSPTRTDVLRLVLYLFTLGPAYAPALPSCKEDEYPVGSECCPKCSPG 60
DB 1 MEPPGDMGPPMRSPTRTDVLRLVLYLFTLGPAYAPALPSCKEDEYPVGSECCPKCSPG 60

DB 1 MEPPGDMGPPMRSPTRTDVLRLVLYLFTLGPAYAPALPSCKEDEYPVGSECCPKCSPG 60
QY 61 YRVKACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTIYODGDHCAACRAVATSSPGQRYQKGTESQDTLQNCNCPGTSPNGTLEECQ 180
DB 121 CSPGHFCTIYODGDHCAACRAVATSSPGQRYQKGTESQDTLQNCNCPGTSPNGTLEECQ 180
QY 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKRKRGVVKVIYS 240
DB 181 HQTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKRKRGVVKVIYS 240
QY 241 VQRKROAEAGETATVIALQAPDVTVAVEETIPSTGSPNH 283
DB 241 VQRKROAEAGETATVIALQAPDVTVAVEETIPSTGSPNH 283

RESULT 6
US-08-462-315-2
Sequence 2, Application US/08462315
GENERAL INFORMATION:
APPLICANT: NI, ET AL.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: June 5, 1995
APPLICATION NUMBER: US/08/462,315
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05058
FILING DATE: 27 APR 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-462-315-2

Query Match 100.0%; Score 1578; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 7,2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSPTRTDVLRLVLYLFTLGPAYAPALPSCKEDEYPVGSECCPKCSPG 60
DB 1 MEPPGDMGPPMRSPTRTDVLRLVLYLFTLGPAYAPALPSCKEDEYPVGSECCPKCSPG 60
QY 61 YRVKACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVCPCPPGTIYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120

QY 121 CSPGHFCTIVODGDHCAACRAVATSSPGORVOKGCTESODTLCONCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCTIVODGDHCAACRAVATSSPGORVOKGCTESODTLCONCPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VOKRQOAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VOKRQOAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 7
US-08-462-962-2
; Sequence 2, Application US/08462962
; GENERAL INFORMATION:
; APPLICANT: NI, ET AL.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,962
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05058
; FILING DATE: 27 APR 95
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-422
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-462-962-2

Query Match 100.0%; Score 1578; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VOKRQOAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VOKRQOAEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 8
US-08-464-595-2
; Sequence 2, Application US/08464595
; GENERAL INFORMATION:
; APPLICANT: JIAN NI, REINER GENTZ AND CRAIG ROSEN
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,595
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05058
; FILING DATE: April 27, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-464-595-2

Query Match 100.0%; Score 1578; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 VORRQOAEAGEATVIEALQAPDPVTTVAVEETIPSTGRSPNH 283

RESULT 9

US-08-741-095B-26
Sequence 26, Application US/08741095B
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-like 2
FILE REFERENCE: 1488.0770004
CURRENT APPLICATION NUMBER: US/08/741,095B
CURRENT FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: US 08/464,595
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/462,962
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/462,315
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: PCT/US95/05058
PRIOR FILING DATE: 1995-04-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-08-741-095B-26

Query Match 100.0%; Score 1578; DB 11; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEYPVGSCECPKCSPG 60
1 MEPPGDMGPPMRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEYPVGSCECPKCSPG 60
Db 1 MEPPGDMGPPMRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEYPVGSCECPKCSPG 60
QY 61 YRVKACGELTGTCVCEPCPGTYIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
61 YRVKACGELTGTCVCEPCPGTYIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
Db 61 YRVKACGELTGTCVCEPCPGTYIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCTVQDDHCAACRAVATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCTVQDDHCAACRAVATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
Db 121 CSPGHFCTVQDDHCAACRAVATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
QY 181 HOTKSWLVTKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIVS 240
181 HOTKSWLVTKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIVS 240
Db 181 HOTKSWLVTKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIVS 240
QY 241 VORRQOAEAGEATVIEALQAPDPVTTVAVEETIPSTGRSPNH 283
241 VORRQOAEAGEATVIEALQAPDPVTTVAVEETIPSTGRSPNH 283
Db 241 VORRQOAEAGEATVIEALQAPDPVTTVAVEETIPSTGRSPNH 283

RESULT 10

US-08-987-902-1
Sequence 1, Application US/08987902
GENERAL INFORMATION:
APPLICANT: Avi J. Aabkenazi and Scot A. Marssters
TITLE OF INVENTION: HIVEN Polypeptides and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,902
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1068R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-5416
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-987-902-1

Query Match 100.0%; Score 1578; DB 13; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEYPVGSCECPKCSPG 60
1 MEPPGDMGPPMRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEYPVGSCECPKCSPG 60
Db 1 MEPPGDMGPPMRSTPRTDVLRLVLYLFTLGAPCYAPALPSCKEDEYPVGSCECPKCSPG 60
QY 61 YRVKACGELTGTCVCEPCPGTYIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
61 YRVKACGELTGTCVCEPCPGTYIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
Db 61 YRVKACGELTGTCVCEPCPGTYIAHLNGLSKLQCOMCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCTVQDDHCAACRAVATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
121 CSPGHFCTVQDDHCAACRAVATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
Db 121 CSPGHFCTVQDDHCAACRAVATSSPGQVQKGTESQDTLQNCPPGTFSPNGTLEECQ 180
QY 181 HOTKSWLVTKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIVS 240
181 HOTKSWLVTKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIVS 240
Db 181 HOTKSWLVTKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDVAVIVS 240
QY 241 VORRQOAEAGEATVIEALQAPDPVTTVAVEETIPSTGRSPNH 283
241 VORRQOAEAGEATVIEALQAPDPVTTVAVEETIPSTGRSPNH 283
Db 241 VORRQOAEAGEATVIEALQAPDPVTTVAVEETIPSTGRSPNH 283

RESULT 11

US-09-342-767-13
Sequence 13, Application US/09342767
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: M81098-061CPI
CURRENT APPLICATION NUMBER: US/09/342,767
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 09/146,950
EARLIER FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(38)
US-09-342-767-13

Query Match 100.0%; Score 1578; DB 17; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPDGMGPPWRSTPRTDVLRLVLYLFTLGAFCYAPALPSCKEDEYVVGSECCPKCSFG 60
DB 1 MPPDGMGPPWRSTPRTDVLRLVLYLFTLGAFCYAPALPSCKEDEYVVGSECCPKCSFG 60
QY 61 YRKEACGELTGTCVCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASNCRSTENAVCG 120
DB 61 YRKEACGELTGTCVCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEBQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDDVVKVIVS 240
DB 181 HOTKCSMLVTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDDVVKVIVS 240
QY 241 VORRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VORRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 12

US-09-480-284-1
; Sequence 1, Application US/09480284
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi and Scot A. Marsters
; TITLE OF INVENTION: HIVM Polypeptides and Uses Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/480,284
; FILING DATE: 10-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/987,902
; FILING DATE: 10-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1068R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-480-284-1

Query Match 100.0%; Score 1578; DB 18; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPPDGMGPPWRSTPRTDVLRLVLYLFTLGAFCYAPALPSCKEDEYVVGSECCPKCSFG 60
DB 1 MPPDGMGPPWRSTPRTDVLRLVLYLFTLGAFCYAPALPSCKEDEYVVGSECCPKCSFG 60
QY 61 YRKEACGELTGTCVCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASNCRSTENAVCG 120
DB 61 YRKEACGELTGTCVCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEBQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDDVVKVIVS 240
DB 181 HOTKCSMLVTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDDVVKVIVS 240
QY 241 VORRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VORRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEBQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDDVVKVIVS 240
DB 181 HOTKCSMLVTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDDVVKVIVS 240
QY 241 VORRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VORRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 13

US-09-533-262-26
; Sequence 26, Application US/09533262
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Genetz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like 2
; FILE REFERENCE: 1488.077000A
; CURRENT APPLICATION NUMBER: US/09/533,262
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: US 60/147,383
; EARLIER FILING DATE: 1999-08-06
; EARLIER APPLICATION NUMBER: US 60/135,169
; EARLIER FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: US 60/126,522
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: US 60/125,683
; EARLIER FILING DATE: 1999-03-22
; EARLIER APPLICATION NUMBER: US 08/741,095
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/464,595
; EARLIER FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 08/462,962
; EARLIER FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 08/462,315
; EARLIER FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: PCT/US95/05058
; EARLIER FILING DATE: 1995-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-533-262-26

Query Match 100.0%; Score 1578; DB 19; Length 283;
Best Local Similarity 100.0%; Pred. No. 7.2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPPDGMGPPWRSTPRTDVLRLVLYLFTLGAFCYAPALPSCKEDEYVVGSECCPKCSFG 60
DB 1 MPPDGMGPPWRSTPRTDVLRLVLYLFTLGAFCYAPALPSCKEDEYVVGSECCPKCSFG 60
QY 61 YRKEACGELTGTCVCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASNCRSTENAVCG 120
DB 61 YRKEACGELTGTCVCEPCPGTYIAHLNGLSKLQCCQCDPAMGLRASNCRSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEBQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDDVVKVIVS 240
DB 181 HOTKCSMLVTAKAGAGTSSSHWMMFLSGSLVIVICSTVGLIICVRRKPRGDDVVKVIVS 240
QY 241 VORRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
DB 241 VORRQEAEGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 14
US-09-791-537-41397
; Sequence 41397, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41397
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-41397
Query March 100.0%; Score 1578; DB 22; Length 283;
Best Local Similarity 100.0%; Pctd. No. 7,2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPPGDGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSPG 60
DB 1 MEPPGDGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEVPGSECCPKCSPG 60
QY 61 YRVKACGELTGVCCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGVCCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVDDGHCACACRAVATSSPQAVQKGTSEODTLCONCPGPTGSPNGTLEECQ 180
DB 121 CSPGHFCTVDDGHCACACRAVATSSPQAVQKGTSEODTLCONCPGPTGSPNGTLEECQ 180
QY 181 HQTKCSLVTKAGAGTSSSHMMWMLSGSLVIVIVGTVGLIICVKKRKRGGVVKIVTS 240
DB 181 HQTKCSLVTKAGAGTSSSHMMWMLSGSLVIVIVGTVGLIICVKKRKRGGVVKIVTS 240
QY 241 VQKROEAGEGATVIEALQAPPDVTVAVEETIPSTFGSRPNH 283
DB 241 VQKROEAGEGATVIEALQAPPDVTVAVEETIPSTFGSRPNH 283

PRIOR FILING DATE: April 29, 1998
PRIOR APPLICATION NUMBER: 60/082,767
PRIOR FILING DATE: April 23, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/066,772
PRIOR FILING DATE: November 24, 1997
PRIOR APPLICATION NUMBER: 60/032,705
PRIOR FILING DATE: December 12, 1996
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: 09/709,238
PRIOR FILING DATE: November 8, 2000
PRIOR APPLICATION NUMBER: 09/664,610
PRIOR FILING DATE: September 18, 2000
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: September 18, 2000
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: August 23, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14941
PRIOR FILING DATE: May 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: May 17, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05004
PRIOR FILING DATE: February 24, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: February 18, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: February 18, 2000
PRIOR APPLICATION NUMBER: 09/480,284
PRIOR FILING DATE: January 10, 2000
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: December 2, 1999
PRIOR APPLICATION NUMBER: 09/423,844
PRIOR FILING DATE: November 12, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: November 30, 1999
PRIOR APPLICATION NUMBER: 09/403,297
PRIOR FILING DATE: October 18, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: September 1, 1999
PRIOR APPLICATION NUMBER: 09/380,137
PRIOR FILING DATE: August 25, 1999
PRIOR APPLICATION NUMBER: 09/380,138
PRIOR FILING DATE: August 25, 1999
PRIOR APPLICATION NUMBER: 09/380,139
PRIOR FILING DATE: August 25, 1999
PRIOR APPLICATION NUMBER: 09/367,206
PRIOR FILING DATE: August 9, 1999
PRIOR APPLICATION NUMBER: 09/369,028
PRIOR FILING DATE: August 4, 1999

;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 2, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/08847
;; PRIOR FILING DATE: April 23, 1999
;; PRIOR APPLICATION NUMBER: 09/298,404
;; PRIOR FILING DATE: April 23, 1999
;; PRIOR APPLICATION NUMBER: 09/284,291
;; PRIOR FILING DATE: April 12, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: March 8, 1999
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/00106
;; PRIOR FILING DATE: January 5, 1999
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: 09/065,275
;; PRIOR FILING DATE: April 23, 1998
;; PRIOR APPLICATION NUMBER: 08/987,902
;; PRIOR FILING DATE: December 10, 1997
;; PRIOR APPLICATION NUMBER: PCT/US97/22278
;; PRIOR FILING DATE: December 5, 1997
;; NUMBER OF SEQ ID NOS: 113
;; SEQ ID NO 46
;; LENGTH: 283
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-882-636-46

Query Match 100.0%; Score 1578; DB 23; Length 283;
Best Local Similarity 100.0%; Pred. No. 7,2e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPDGMGPPPPRSTPRDVLRLVLTFLGAPCYAPALPSCKEDEYVGSRCPCSPG 60
DB 1 MEPPDGMGPPPPRSTPRDVLRLVLTFLGAPCYAPALPSCKEDEYVGSRCPCSPG 60
QY 61 YRVKACGELTGTVECPPTGYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGTVECPPTGYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDDGHCACRAVATSSPGQVQKGTESQDILQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQDDGHCACRAVATSSPGQVQKGTESQDILQNCPPGTFSPNGTLEECQ 180
QY 181 HOTKCSWLVYTAGAGTSSSHWFWFLSGSLVIVYCVSTVGLIICVRRKPRGDVVKVIVS 240
DB 181 HOTKCSWLVYTAGAGTSSSHWFWFLSGSLVIVYCVSTVGLIICVRRKPRGDVVKVIVS 240
QY 241 VORKROEAGEATVIEALQAPPDVTVAEETIPSTGRSPWH 283
DB 241 VORKROEAGEATVIEALQAPPDVTVAEETIPSTGRSPWH 283

Search completed: November 14, 2003, 17:35:59
Job time : 176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 17:30:56 ; Search time 20 Seconds
(without alignment)
683.668 Million cell updates/sec

Title: US-08-741-095B-26
Perfect score: 1578
Sequence: 1 MEBPGDWGPPMRSTPRTDY.....VTVAVEETIPSTGSRPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 255527 seqs, 4815734 residues

Total number of hits satisfying chosen parameters: 255527

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_US02_29560A-288
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pcp:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pcp:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pcp:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pcp:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pcp:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1578	100.0	283	1 PCT-US02-29560A-288	Sequence 288, App
2	1575	99.8	283	6 US-10-322-281-546	Sequence 546, App
3	1575	99.8	283	6 US-10-322-281-548	Sequence 548, App
4	1575	99.8	283	6 US-10-322-281-550	Sequence 550, App
5	1575	99.8	283	7 US-60-512-690-303	Sequence 303, App
6	1575	99.8	283	7 US-60-512-690-304	Sequence 304, App
7	1575	99.8	283	7 US-60-512-690-305	Sequence 305, App
8	1575	99.8	283	7 US-60-512-690-306	Sequence 306, App
9	1477	93.6	282	1 PCT-US03-28227-3157	Sequence 3157, App
10	1477	93.6	282	1 PCT-US03-28227-3158	Sequence 3158, App
11	1477	93.6	282	1 PCT-US03-28227-3159	Sequence 3159, App
12	1477	93.6	282	1 PCT-US03-28227-3160	Sequence 3160, App
13	1477	93.6	282	1 PCT-US03-28227-3161	Sequence 3161, App
14	990	62.7	199	7 US-60-512-690-308	Sequence 308, App
15	787	49.9	172	7 US-60-512-690-307	Sequence 307, App
16	384.5	24.4	194	6 US-10-322-281-543	Sequence 543, App
17	267.5	17.0	277	1 PCT-US02-29560A-281	Sequence 281, App
18	267.5	17.0	277	1 PCT-US03-32827-28	Sequence 28, App1
19	267.5	17.0	277	5 US-09-467-317-2	Sequence 2, App1
20	267.5	17.0	277	6 US-10-688-845-28	Sequence 323, App
21	264.5	16.8	431	1 PCT-US03-28227-3326	Sequence 3226, App
22	259	16.4	182	4 US-08-484-783B-14	Sequence 14, App1
23	259	16.4	184	4 US-08-484-783B-15	Sequence 15, App1
24	259	16.4	235	4 US-08-484-783B-13	Sequence 13, App1
25	259	16.4	235	5 US-09-882-735A-16	Sequence 16, App1
26	259	16.4	235	5 US-09-882-735A-16	Sequence 16, App1

27	259	16.4	461	1 PCT-US03-31974-32	Sequence 32, App1
28	259	16.4	461	4 US-08-484-783B-12	Sequence 12, App1
29	259	16.4	461	6 US-10-456-819-17	Sequence 17, App1
30	259	16.4	461	7 US-60-487-610-2160	Sequence 2160, App
31	258.5	16.4	193	6 US-10-328-953-318	Sequence 318, App1
32	256	16.2	218	5 US-09-569-611C-33	Sequence 33, App1
33	256	16.2	218	5 US-09-569-611B-33	Sequence 33, App1
34	256	16.2	218	5 US-09-569-611C-33	Sequence 33, App1
35	253	16.0	435	1 PCT-US03-24669-353	Sequence 353, App
36	253	16.0	446	1 PCT-US03-28227-3859	Sequence 3859, App
37	253	16.0	450	1 PCT-US03-24669-354	Sequence 354, App
38	247.5	15.7	439	1 PCT-US03-28227-3860	Sequence 3860, App
39	246	15.6	300	1 PCT-US02-29560A-230	Sequence 230, App
40	246	15.6	300	1 PCT-US02-29560A-231	Sequence 231, App
41	246	15.6	300	6 US-10-456-819-1	Sequence 1, App1
42	240	15.2	399	1 PCT-US03-24669-352	Sequence 352, App
43	240	15.2	410	1 PCT-US03-28227-3861	Sequence 3861, App
44	240	15.2	635	1 PCT-US03-24669-355	Sequence 355, App
45	239	15.1	305	1 PCT-US03-24669-357	Sequence 357, App

ALIGNMENTS

RESULT 1
PCT-US02-29560A-288
Sequence 288, Application PC/TUS0229560A
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezl, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Wilson, Keith E.
APPLICANT: Zlotnik, Albert
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer. Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710PC
CURRENT APPLICATION NUMBER: PCT/US02/29560A
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 412
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 288
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-29560A-288
Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 4.8e-55;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MEBPGDWGPPMRSTPRTDYLVLTFLGAPCAVAPALPSCDEDEYVPGSECCPCSPG 60
1 MEBPGDWGPPMRSTPRTDYLVLTFLGAPCAVAPALPSCDEDEYVPGSECCPCSPG 60
61 YVKEACGSLTGVCEPCPGTYIAHLNGLSKLOCOMDPAMGLASRNCRSTENAVCG 120
61 YVKEACGSLTGVCEPCPGTYIAHLNGLSKLOCOMDPAMGLASRNCRSTENAVCG 120
61 YVKEACGSLTGVCEPCPGTYIAHLNGLSKLOCOMDPAMGLASRNCRSTENAVCG 120
121 CSPGHFICVODGDHCAACRAVATSSPGQVQKGTESQDTLCNCPGTFSPGNTLEBQ 180
121 CSPGHFICVODGDHCAACRAVATSSPGQVQKGTESQDTLCNCPGTFSPGNTLEBQ 180
121 CSPGHFICVODGDHCAACRAVATSSPGQVQKGTESQDTLCNCPGTFSPGNTLEBQ 180
181 HQTCKSWLTKAGACGSSHHWWFLSGSLVIVICSTYGLIICVRRKRPDGVAVIYS 240
181 HQTCKSWLTKAGACGSSHHWWFLSGSLVIVICSTYGLIICVRRKRPDGVAVIYS 240
241 VQRKQEAEGEATVLEAQPDPVTVVAVEETIPSTGSRPNH 283
241 VQRKQEAEGEATVLEAQPDPVTVVAVEETIPSTGSRPNH 283

Db 241 VORKEAGEATVIEALQAPDVTVAEETIPSTGRSPNH 283

RESULT 2

US-10-322-281-546

; Sequence 546, Application US/10322281

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc S. Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001000

; CURRENT APPLICATION NUMBER: US/10/322,281

; CURRENT FILING DATE: 2002-12-17

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 546

; LENGTH: 283

; TYPE: PRF

; ORGANISM: Homo sapiens

US-10-322-281-546

Query Match

99.8%; Score 1575; DB 6; Length 283;

Best Local Similarity 99.6%; Pred. No. 6.3e-55;

Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPDGMGPPMRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECPKCSFG 60

Db 1 MEPPDGMGPPMRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECPKCSFG 60

QY 61 YRKEACGELTGTCCEPCEPGTYIAHLNGLSKLCQCMCDPAMGLRASNCSRTENAVCG 120

Db 61 YRKEACGELTGTCCEPCEPGTYIAHLNGLSKLCQCMCDPAMGLRASNCSRTENAVCG 120

QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEBQ 180

Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEBQ 180

QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVCSVGLIICVRRKPRGDVVKVIVS 240

Db 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVCSVGLIICVRRKPRGDVVKVIVS 240

QY 241 VORKEAGEATVIEALQAPDVTVAEETIPSTGRSPNH 283

Db 241 VORKEAGEATVIEALQAPDVTVAEETIPSTGRSPNH 283

RESULT 3

US-10-322-281-548

; Sequence 548, Application US/10322281

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc S. Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001000

; CURRENT APPLICATION NUMBER: US/10/322,281

; CURRENT FILING DATE: 2002-12-17

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 548

; LENGTH: 283

; TYPE: PRF

; ORGANISM: Homo sapiens

US-10-322-281-548

Query Match

99.8%; Score 1575; DB 6; Length 283;

Best Local Similarity 99.6%; Pred. No. 6.3e-55;

Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPDGMGPPMRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECPKCSFG 60

Db 1 MEPPDGMGPPMRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECPKCSFG 60

QY 61 YRKEACGELTGTCCEPCEPGTYIAHLNGLSKLCQCMCDPAMGLRASNCSRTENAVCG 120

Db 61 YRKEACGELTGTCCEPCEPGTYIAHLNGLSKLCQCMCDPAMGLRASNCSRTENAVCG 120

Db 61 YRKEACGELTGTCCEPCEPGTYIAHLNGLSKLCQCMCDPAMGLRASNCSRTENAVCG 120

QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEBQ 180

Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEBQ 180

QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVCSVGLIICVRRKPRGDVVKVIVS 240

Db 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVCSVGLIICVRRKPRGDVVKVIVS 240

QY 241 VORKEAGEATVIEALQAPDVTVAEETIPSTGRSPNH 283

Db 241 VORKEAGEATVIEALQAPDVTVAEETIPSTGRSPNH 283

RESULT 4

US-10-322-281-550

; Sequence 550, Application US/10322281

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc S. Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001000

; CURRENT APPLICATION NUMBER: US/10/322,281

; CURRENT FILING DATE: 2002-12-17

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 550

; LENGTH: 283

; TYPE: PRF

; ORGANISM: Homo sapiens

US-10-322-281-550

Query Match

99.8%; Score 1575; DB 6; Length 283;

Best Local Similarity 99.6%; Pred. No. 6.3e-55;

Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPDGMGPPMRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECPKCSFG 60

Db 1 MEPPDGMGPPMRSTPRDVLRLVLYLTLFLGAPCAAPALPSCKEDEYVGSCECPKCSFG 60

QY 61 YRKEACGELTGTCCEPCEPGTYIAHLNGLSKLCQCMCDPAMGLRASNCSRTENAVCG 120

Db 61 YRKEACGELTGTCCEPCEPGTYIAHLNGLSKLCQCMCDPAMGLRASNCSRTENAVCG 120

QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEBQ 180

Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESQDTLCQNCPPGTFSPNGTLEBQ 180

QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVCSVGLIICVRRKPRGDVVKVIVS 240

Db 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVCSVGLIICVRRKPRGDVVKVIVS 240

QY 241 VORKEAGEATVIEALQAPDVTVAEETIPSTGRSPNH 283

Db 241 VORKEAGEATVIEALQAPDVTVAEETIPSTGRSPNH 283

RESULT 5

US-60-512-690-303

; Sequence 303, Application US/60512690

; GENERAL INFORMATION:

; APPLICANT: DOMON, Bruno

; APPLICANT: HE, Tao

; APPLICANT: LI, Aigun

; APPLICANT: ZHANG, Xiaolong

; APPLICANT: KETCHUM, Karen

; APPLICANT: MCCAFFERY, Ian

; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES

; FILE REFERENCE: CLO01478PROV

US-60-512-690-303

QY 241 VORKEAGEATVIEALQAPDVTVAEETIPSTGRSPNH 283

Db 241 VORKEAGEATVIEALQAPDVTVAEETIPSTGRSPNH 283

```
; CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-512-690-303
```

```
Query Match          99.8%; Score 1575; DB 7; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MEBPGDWGPPPMSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60
DB 1 MEBPGDWGPPPMSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60
QY 61 YRVKACGELTGVCBPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGVCBPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKPRGDVAVYVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKPRGDVAVYVS 240
QY 241 VOKRQAEAGEATVIEALQAPDVTTVAAVEETIPSFGRSPNH 283
DB 241 VOKRQAEAGEATVIEALQAPDVTTVAAVEETIPSFGRSPNH 283
```

```
RESULT 6
US-60-512-690-304
; Sequence 304, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Aiqun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: MCCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
; FILE REFERENCE: CL001478PROV
; CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-512-690-304
```

```
Query Match          99.8%; Score 1575; DB 7; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MEBPGDWGPPPMSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60
DB 1 MEBPGDWGPPPMSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60
QY 61 YRVKACGELTGVCBPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGVCBPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
```

```
DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKPRGDVAVYVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKPRGDVAVYVS 240
QY 241 VOKRQAEAGEATVIEALQAPDVTTVAAVEETIPSFGRSPNH 283
DB 241 VOKRQAEAGEATVIEALQAPDVTTVAAVEETIPSFGRSPNH 283
```

```
RESULT 7
US-60-512-690-305
; Sequence 305, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Aiqun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: MCCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
; FILE REFERENCE: CL001478PROV
; CURRENT APPLICATION NUMBER: US/60/512,690
; CURRENT FILING DATE: 2003-10-23
; NUMBER OF SEQ ID NOS: 1027
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-512-690-305
```

```
Query Match          99.8%; Score 1575; DB 7; Length 283;
Best Local Similarity 99.6%; Pred. No. 6.3e-55;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MEBPGDWGPPPMSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60
DB 1 MEBPGDWGPPPMSTRTDVLRLVLYTLFLGAPCYAPALPSCKEDEYPVGSECCPKCSPG 60
QY 61 YRVKACGELTGVCBPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGVCBPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKPRGDVAVYVS 240
DB 181 HOTKCSMLVTYKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVRRKPRGDVAVYVS 240
QY 241 VOKRQAEAGEATVIEALQAPDVTTVAAVEETIPSFGRSPNH 283
DB 241 VOKRQAEAGEATVIEALQAPDVTTVAAVEETIPSFGRSPNH 283
```

```
RESULT 8
US-60-512-690-306
; Sequence 306, Application US/60512690
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno
; APPLICANT: HE, Tao
; APPLICANT: LI, Aiqun
; APPLICANT: ZHANG, Xiaolong
; APPLICANT: KETCHUM, Karen
; APPLICANT: MCCAFFERY, Ian
; APPLICANT: NARAYAN, Vaibhav
; TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
; FILE REFERENCE: THEROOF
```

```
FILE REFERENCE: CL001478PROV
CURRENT APPLICATION NUMBER: US/60/512,690
CURRENT FILING DATE: 2003-10-23
NUMBER OF SEQ ID NOS: 1027
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 306
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-60-512-690-306

Query Match
Best Local Similarity 99.8%; Score 1575; DB 7; Length 283;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPGDWGPWPWRSTPRTDVLRLVLYLTFLGAPCAPALPSCKEDEYVPGSECCPKCSPG 60
DB 1 MPPGDWGPWPWRSTPRTDVLRLVLYLTFLGAPCAPALPSCKEDEYVPGSECCPKCSPG 60
QY 61 YVKEACGELTGVCCEPPTGYIAHLNGLSKLCQCCDPMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGVCCEPPTGYIAHLNGLSKLCQCCDPMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVOKGTESDTLQONCPPTFSFNGTLEECQ 180
DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVOKGTESDTLQONCPPTFSFNGTLEECQ 180
QY 181 HOTKCSMLVTKAGAGTSSSHWWWWFLSGSLVIVICSTVGLIICVKKRRPRGDDVVKIVS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWWWFLSGSLVIVICSTVGLIICVKKRRPRGDDVVKIVS 240
QY 241 VOKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
DB 241 VOKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283

RESULT 9
PCT-US03-28227-3157
Sequence 3157, Application PC/TUS0328227
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, Toineette A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STUVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: XU, Yuning; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PN-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEQ ID NO 3157
```

```
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 928524.FT115P
PCT-US03-28227-3157

Query Match
Best Local Similarity 99.2%; Score 1477; DB 1; Length 282;
Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPGDWGPWPWRSTPRTDVLRLVLYLTFLGAPCAPALPSCKEDEYVPGSECCPKCSPG 60
DB 1 MPPGDWGPWPWRSTPRTDVLRLVLYLTFLGAPCAPALPSCKEDEYVPGSECCPKCSPG 60
QY 61 YVKEACGELTGVCCEPPTGYIAHLNGLSKLCQCCDPMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGVCCEPPTGYIAHLNGLSKLCQCCDPMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVOKGTESDTLQONCPPTFSFNGTLEECQ 180
DB 121 CSPGHFCIVQDGDHCAACRAVATSSPGQVOKGTESDTLQONCPPTFSFNGTLEECQ 180
QY 181 HOTKCSMLVTKAGAGTSSSHWWWWFLSGSLVIVICSTVGLIICVKKRRPRGDDVVKIVS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWWWFLSGSLVIVICSTVGLIICVKKRRPRGDDVVKIVS 240
QY 241 VOKRQEAEGEATVIEALQAPPDVT 265
DB 241 VOKRQEAEGEATVIEALQAPPDAT 265

RESULT 10
PCT-US03-28227-3158
Sequence 3158, Application PC/TUS0328227
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, Toineette A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STUVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: XU, Yuning; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PN-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEQ ID NO 3158
TYPE: PRT
ORGANISM: Homo sapiens
```

FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 928524.PT117P
PCT-US03-28227-3158

Query Match 93.6%; Score 1477; DB 1; Length 282;
Best Local Similarity 99.2%; Pred. No. 3.8e-51;
Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMPPRMRSTPTDVLRLVLYLFLGAPCYALPSCKEDEYVSGCCPKSPG 60
DB 1 MEPPGDMPPRMRSTPTDVLRLVLYLFLGAPCYALPSCKEDEYVSGCCPKSPG 60
QY 61 YRVKACGELTGYCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGYCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTSPNGTLEECQ 180
QY 181 HOTKCSWLTKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKRRKRGDVVKYIVS 240
DB 181 HOTKCSWLTKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKRRKRGDVVKYIVS 240
QY 241 VQRKQAEAGEATVIEALQAPPDVT 265
DB 241 VQRKQAEAGEATVIEALQAPPDAT 265

RESULT 11

PCT-US03-28227-3159
Sequence 3159, Application PC/TUS0328227
GENERAL INFORMATION:

APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyana H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STUVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: XU, Yuming; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PN-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEQ ID NO 3159
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 928524.PT130P

PCT-US03-28227-3159

Query Match 93.6%; Score 1477; DB 1; Length 282;
Best Local Similarity 99.2%; Pred. No. 3.8e-51;
Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPPGDMPPRMRSTPTDVLRLVLYLFLGAPCYALPSCKEDEYVSGCCPKSPG 60
DB 1 MEPPGDMPPRMRSTPTDVLRLVLYLFLGAPCYALPSCKEDEYVSGCCPKSPG 60
QY 61 YRVKACGELTGYCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
DB 61 YRVKACGELTGYCEPCPGTYIAHLNGLSKLCQCMCDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCTVODGDHCAACRAVATSSPGQVQKGTESQDTLCONCPGTSPNGTLEECQ 180
QY 181 HOTKCSWLTKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKRRKRGDVVKYIVS 240
DB 181 HOTKCSWLTKAGAGTSSSHWWMFLSGSLVIYIVCSTVGLIICVKRRKRGDVVKYIVS 240
QY 241 VQRKQAEAGEATVIEALQAPPDVT 265
DB 241 VQRKQAEAGEATVIEALQAPPDAT 265

RESULT 12

PCT-US03-28227-3160
Sequence 3160, Application PC/TUS0328227
GENERAL INFORMATION:

APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEGANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyana H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STUVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: XU, Yuming; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PN-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEQ ID NO 3160
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 928524.PT139P
PCT-US03-28227-3160

Query Match 93.6%; Score 1477; DB 1; Length 282;

Best Local Similarity 99.2%; Pred. No. 3.8e-51;
Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPGDMGPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
DB 1 MPPGDMGPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
QY 61 YRKEACGELTGVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLASRNCSTENAVCG 120
DB 61 YRKEACGELTGVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLASRNCSTENAVCG 120
QY 121 CSFGHFCIVQDDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
DB 121 CSFGHFCIVQDDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTKAGAGTSSSHWWMFSLGSLVIVICSTVGLIICVRRKPRGDVVKIVIS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWMFSLGSLVIVICSTVGLIICVRRKPRGDVVKIVIS 240
QY 241 VORKEOAEAGTATVIEALQAPPDVT 265
DB 241 VORKEOAEAGTATVIEALQAPPDVT 265

RESULT 13

PCT-US03-28227-3161
Sequence 3161, Application PC/TUS0328227

GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;
APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;
APPLICANT: MARJANOVIC, Mirjana M.; SHEN, Fan;
APPLICANT: HARTSHORNE, ToINETTE A.; SUCHOROLSKI, Martin;
APPLICANT: ALTUS, Christina M.; PITTS, Steven J.;
APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;
APPLICANT: DELEBANE, Angelo M.; PANESAR, Iqbal S.;
APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;
APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;
APPLICANT: PANZER, Scott R.; WANG, Xinhao;
APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;
APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;
APPLICANT: RIOUX, Pierre; SHEN, Edward J.;
APPLICANT: WU, Mingham C.; STUVE, Laura L.;
APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;
APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;
APPLICANT: VITT, Ursula A.; KIRTON, Edward;
APPLICANT: XU, Yuming; KWONG, Mary;
APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;
APPLICANT: MA, Yan; JACKSON, Jennifer L.;
APPLICANT: GIETZEN, Darryl; PATURY, Srikanth;
APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PR-0100 PCT
CURRENT APPLICATION NUMBER: PCT/US03/28227
PRIOR FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/410,260
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/410,259
PRIOR FILING DATE: 2002-09-12
NUMBER OF SEQ ID NOS: 5444
SOFTWARE: PERL Program
SEO ID NO 3161
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 928524.PT146p
PCT-US03-28227-3161

Query Match 93.6%; Score 1477; DB 1; Length 282;
Best Local Similarity 99.2%; Pred. No. 3.8e-51;
Matches 263; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPGDMGPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
DB 1 MPPGDMGPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYVGSSECCPKCSFG 60
QY 61 YRKEACGELTGVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLASRNCSTENAVCG 120
DB 61 YRKEACGELTGVCEPCPGTYIAHLNGLSKLCQCMCDPAMGLASRNCSTENAVCG 120
QY 121 CSFGHFCIVQDDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
DB 121 CSFGHFCIVQDDHCAACRAVATSSPGQVQKGTESODTLQNCPPGTFSPNGTLEBQ 180
QY 181 HOTKCSMLVTKAGAGTSSSHWWMFSLGSLVIVICSTVGLIICVRRKPRGDVVKIVIS 240
DB 181 HOTKCSMLVTKAGAGTSSSHWWMFSLGSLVIVICSTVGLIICVRRKPRGDVVKIVIS 240
QY 241 VORKEOAEAGTATVIEALQAPPDVT 265
DB 241 VORKEOAEAGTATVIEALQAPPDVT 265

RESULT 14

US-60-512-690-308
Sequence 308, Application US/60512690

GENERAL INFORMATION:
APPLICANT: DOMON, Bruno
APPLICANT: HE, Tao
APPLICANT: LI, Aigun
APPLICANT: ZHANG, Xiaolong
APPLICANT: KETCHUM, Karen
APPLICANT: MCCAFFERY, Ian
APPLICANT: NARAYAN, Vaibhav
TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
FILE REFERENCE: CL001478PROV
CURRENT APPLICATION NUMBER: US/60/512,690
PRIOR FILING DATE: 2003-10-23
NUMBER OF SEQ ID NOS: 1027
SOFTWARE: FastSeq for Windows Version 4.0
SEO ID NO 308
LENGTH: 199
TYPE: PRT
ORGANISM: Homo sapiens
US-60-512-690-308

Query Match 62.7%; Score 990; DB 7; Length 199;
Best Local Similarity 100.0%; Pred. No. 2e-32;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 PAMGLASRNCSTENAVCGSPGHFCIVQDDHCAACRAVATSSPGQVQKGTESODT 160
DB 17 PAMGLASRNCSTENAVCGSPGHFCIVQDDHCAACRAVATSSPGQVQKGTESODT 76
QY 161 LQNCPPGTFSPNGTLEBQHOTKCSMLVTKAGAGTSSSHWWMFSLGSLVIVICSTVG 220
DB 77 LQNCPPGTFSPNGTLEBQHOTKCSMLVTKAGAGTSSSHWWMFSLGSLVIVICSTVG 136
QY 221 LIIICVRRKPRGDVVKIVISVORKEOAEAGTATVIEALQAPPDVTVAEETIPSTGRS 280
DB 137 LIIICVRRKPRGDVVKIVISVORKEOAEAGTATVIEALQAPPDVTVAEETIPSTGRS 196
QY 281 PNH 283
DB 197 PNH 199

RESULT 15

US-60-512-690-307
Sequence 307, Application US/60512690

GENERAL INFORMATION:
APPLICANT: DOMON, Bruno
APPLICANT: HE, Tao
APPLICANT: LI, Aigun

APPLICANT: ZHANG, Xiaolong
APPLICANT: KETCHUM, Karen
APPLICANT: MCCAFFERY, Ian
APPLICANT: NARAYAN, Vaibhav
TITLE OF INVENTION: PANCREATIC DISEASE TARGETS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001478PROV
CURRENT APPLICATION NUMBER: US/60/512,690
CURRENT FILING DATE: 2003-10-23
NUMBER OF SEQ ID NOS: 1027
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 307
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-60-512-690-307

Query Match 49.9%; Score 787; DB 7; Length 172;
Best Local Similarity 99.3%; Pred. No. 1.2e-24;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	101	PAMGLRASNCRSTENAVCGSPGHFCIVDDGDHCAACRAVATSSPGORVOKGSTESQDT	160
DB	17	PAMGLRASNCRSTENAVCGSPGHFCIVDDGDHCAACRAVATSSPGORVOKGSTESQDT	76
QY	161	LCQNCPPGTSPNGTLEECOHQTKCSWLVTYKAGAGTSSSHWVWFLSGSLVIVVCSTVG	220
DB	77	LCQNCPPGTSPNGTLEECOHQTKCSWLVTYKAGAGTSSSHWVWFLSGSLVIVVCSTVG	136
QY	221	LIICVKRRKPRGDVVKIVSVQAK	244
DB	137	LIICVKRRKPRGDVVKIVSVQAK	160

Search completed: November 14, 2003, 17:36:32
Job time : 21 secs

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27. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like 2 protein comprising amino acids 1 to 245 of SEQ ID NO:26.
28. The isolated protein of claim 27, which comprises amino acids -38 to 245 of SEQ ID NO:26.
29. The isolated protein of claim 27, which is produced by a recombinant host cell.
30. The isolated protein of claim 27, which comprises a heterologous polypeptide.
31. The isolated protein of claim 30, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.
32. (amended) A composition comprising the isolated protein of claim 27 and a carrier.
33. (amended) An isolated protein comprising 30 contiguous amino acids of the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059, wherein said 30 contiguous amino acids comprises an antigenic determinant for the polypeptide consisting of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059.
34. The isolated protein of claim 33, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059.
35. The isolated protein of claim 33, which is produced by a recombinant host cell.
36. The isolated protein of claim 33, which comprises a heterologous polypeptide.
37. The isolated protein of claim 36, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.
38. (amended) A composition comprising the isolated protein of claim 33 and carrier.
45. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like protein comprising the mature amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.
46. The isolated protein of claim 45, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.
47. The isolated protein of claim 45, which is produced by a recombinant host cell.
48. The isolated protein of claim 45, which comprises a heterologous polypeptide.
49. The isolated protein of claim 48, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.
50. (amended) A composition comprising the isolated protein of claim 45 and a carrier.
57. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like protein comprising the mature amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

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58. The isolated protein of claim 57, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

59. The isolated protein of claim 57, which is produced by a recombinant host cell.

60. The isolated protein of claim 57, which comprises a heterologous polypeptide.

61. The isolated protein of claim 60, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

62. (amended) A composition comprising the isolated protein of claim 57 and a carrier.

81. (Once Amended) An isolated Human Tumor Necrosis Factor Receptor-Like 2 protein comprising amino acids 1 to 162 of SEQ ID NO:26.

82. The isolated protein of claim 81, which comprises amino acids -38 to 162 of

SEQ ID NO:26.

83. The isolated protein of claim 81, which is produced by a recombinant host cell.

84. The isolated protein of claim 81, which comprises a heterologous polypeptide.

85. The isolated protein of claim 84, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

86. (amended) A composition comprising the isolated protein of claim 81 and a

175. (new) An isolated protein comprising 30 contiguous amino acids of the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058, wherein said 30 contiguous amino acids comprises an antigenic determinant or the polypeptide consisting of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.

176. (new) The isolated protein of claim 175, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97058.

177. (new) The isolated protein of claim 175, which is produced by a recombinant host cell.

178. (new) The isolated protein of claim 175, which comprises a heterologous polypeptide.

179. (new) The isolated protein of claim 178, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

180. (new) A composition comprising the isolated protein of claim 175 and a carrier.

carrier.

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complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057, wherein said 30 contiguous amino acids comprises an antigenic determinant or the polypeptide consisting of the amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

182. (new) The isolated protein of claim 181, which comprises the complete amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97057.

183. (new) The isolated protein of claim 181, which is produced by a recombinant host cell.

184. (new) The isolated protein of claim 181, which comprises a heterologous polypeptide.

185. (new) The isolated protein of claim 184, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

186. (new) A composition comprising the isolated protein of claim 181 and a carrier.

polypeptide consisting of the amino acid sequence of SEQ ID NO: 26, wherein said 30 contiguous amino acids comprises an antigenic determinant for the polypeptide consisting of the amino acid sequence of SEQ ID NO: 26.

188. (new) The isolated protein of claim 187, which is produced by a recombinant host cell.

189. (new) The isolated protein of claim 187, which comprises a heterologous polypeptide.

190. (new) The isolated protein of claim 189, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

191. (new) A composition comprising the isolated protein of claim 187 and a carrier.

192. (new) An isolated protein comprising the mature amino acid sequence encoded by the cDNA clone contained in ATCC Deposit No. 97059.

193. (new) The isolated protein of claim 192, which is produced by a recombinant host cell.

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194. (new) The isolated protein of claim 192, which comprises a heterologous polypeptide.

195. (new) The isolated protein of claim 194, wherein said a heterologous polypeptide comprises the Fc portion of an antibody molecule.

196. (new) A composition comprising the isolated protein of claim 192 and a carrier.

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41. (amended) An isolated antibody which specifically binds to a polypeptide consisting of amino acids -38 to 245 of SEQ ID No. 26. 01/533262 NJ

42. (Once amended) The isolated antibody of claim 41, wherein said antibody is monoclonal antibody.

43. (Once amended) The isolated antibody of claim 41, wherein said antibody is polyclonal antibody.

44. (Once amended) The isolated antibody of claim 41, wherein said antibody is chimeric antibody.

45. (Once amended) The isolated antibody of claim 41, wherein said antibody is humanized antibody.

46. (Once amended) The isolated antibody of claim 41, wherein said antibody is single-chain Fv antibody.

47. (Once amended) The isolated antibody of claim 41, wherein said antibody is Fab antibody fragment.

A composition comprising the Ab of claim 41 and a pharmaceutically acceptable carrier.

60. (New) The isolated antibody of claim 41, wherein said antibody is the product of an Fab expression library.

61. (amended) A method of producing the isolated antibody of claim 41, comprising immunizing an animal with a polypeptide comprising amino acids -38 to 245 of SEQ ID No.

and recovering an antibody, which specifically binds, said polypeptide.

62. (New) A hybridoma which produces the monoclonal antibody of claim 42.

63. (New) A method of producing a monoclonal antibody which comprises:
(a) culturing the hybridoma of claim 62 under appropriate conditions; and

(b) isolating monoclonal antibody therefrom.

64. (amended) An isolated antibody which specifically binds to a polypeptide consisting of amino acids -38 to 162 of SEQ ID No. 26.

65. (New) The isolated antibody of claim 64, wherein said antibody is a monoclonal antibody.

66. (New) The isolated antibody of claim 64, wherein said antibody is a polyclonal antibody.

67. (New) The isolated antibody of claim 64, wherein said antibody is a chimeric antibody.

68. (New) The isolated antibody of claim 64, wherein said antibody is a humanized antibody.

69. (New) The isolated antibody of claim 64, wherein said antibody is a single-chain Fv antibody.

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100. (amended) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 90% identical to amino acids 1 to 162 of SEQ ID NO: 26, wherein said polypeptide inhibits T cell proliferation.

187. The polynucleotide of claim 186, wherein the sequence of said amino acid sequence is at least 90% identical to amino acids -38 to 162 of SEQ ID NO:26.

188. A method of producing a vector which comprises inserting the polynucleotide of claim 186 into a vector.

189. A vector comprising the polynucleotide of claim 186.

190. A host cell comprising the polynucleotide of claim 186 operably associated with a heterologous regulatory element.

191. A method of producing a polypeptide which comprises culturing the host cell of claim 190 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

192. (amended) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 95% identical to amino acids 1 to 162 of SEQ ID NO: 26, wherein said polypeptide inhibits T cell proliferation.

193. The polynucleotide of claim 192, wherein the sequence of said amino acid sequence is at least 95% identical to amino acids -38 to 162 of SEQ ID NO:26.

194. A method of producing a vector which comprises inserting the polynucleotide of claim 192 into a vector.

195. A vector comprising the polynucleotide of claim 192.

196. A host cell comprising the polynucleotide of claim 192 operably associated with a heterologous regulatory element.

197. A method of producing a polypeptide which comprises culturing the host cell of claim 196 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

198. An isolated polynucleotide comprising a nucleic acid encoding amino acids 1 to 162 of SEQ ID NO:26.

199. The polynucleotide of claim 198, comprising nucleotides 123 to 608 of SEQ ID NO:25.

200. The polynucleotide of claim 198, comprising a nucleic acid encoding amino acids -38 to 162 of SEQ ID NO:26.

201. The polynucleotide of claim 200, comprising nucleotides 9 to 608 of SEQ ID NO:25.

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84. (New) A composition comprising the antibody of claim 76 and a pharmaceutically acceptable carrier.

85. (amended) A method of producing the isolated antibody of claim 76, comprising:
(a) immunizing an animal with a polypeptide comprising amino acids 1 to 162 of SEQ ID No. 26; and

(b) recovering an antibody, which specifically binds, said polypeptide.

86. (New) A hybridoma which produces the monoclonal antibody of claim 77.

87. (New) A method of producing a monoclonal antibody which comprises:
(a) culturing the hybridoma of claim 86 under appropriate conditions; and

(b) isolating monoclonal antibody therefrom.

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70. (New) The isolated antibody of claim 64, wherein said antibody is an Fab antibody fragment.

71. (New) The isolated antibody of claim 64, wherein said antibody is the product of an Fab expression library.

72. (New) A composition comprising the antibody of claim 64 and a pharmaceutically acceptable carrier.

73. (amended) A method of producing the isolated antibody of claim 64, comprising:

(a) immunizing an animal with a polypeptide comprising amino acids -38 to 162 of SEQ ID No. 26; and

(b) recovering an antibody which specifically binds said polypeptide.

74. (New) A hybridoma which produces the monoclonal antibody of claim 65.

75. (New) A method of producing a monoclonal antibody which comprises:

(a) culturing the hybridoma of claim 74 under appropriate conditions; and

(b) isolating monoclonal antibody therefrom.

77. (New) The isolated antibody of claim 76, wherein said antibody is a monoclonal antibody.

78. (New) The isolated antibody of claim 76, wherein said antibody is a polyclonal antibody.

79. (New) The isolated antibody of claim 76, wherein said antibody is a chimeric antibody.

80. (New) The isolated antibody of claim 76, wherein said antibody is a humanized antibody.

81. (New) The isolated antibody of claim 76, wherein said antibody is a single-chain Fv antibody.

82. (New) The isolated antibody of claim 76, wherein said antibody is an Fab antibody fragment.

83. (New) The isolated antibody of claim 76, wherein said antibody is the product of an Fab expression library.

consisting of amino acids 1 to 162 of SEQ ID No. 26.

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202. A method of producing a vector which comprises inserting the polynucleotide of claim 198 into a vector.

203. A vector comprising the polynucleotide of claim 198.

204. A host cell comprising the polynucleotide of claim 198 operably associated with a heterologous regulatory element.

205. A method of producing a polypeptide which comprises culturing the host cell of claim 204 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

206. (amended) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 90% identical to amino acids 1 to 245 of SEQ ID NO: 26, wherein said polypeptide stimulates T cell proliferation.

207. The polynucleotide of claim 206, wherein the sequence of said amino acid sequence is at least 90% identical to amino acids -38 to 245 of SEQ ID NO:26.

208. A method of producing a vector which comprises inserting the polynucleotide of claim 206 into a vector.

209. A vector comprising the polynucleotide of claim 206.

210. A host cell comprising the polynucleotide of claim 206 operably associated with a heterologous regulatory element.

211. A method of producing a polypeptide which comprises culturing the host cell of claim 210 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

212. (amended) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising an amino acid sequence at least 95% identical to amino acids 1 to 245 of SEQ ID NO: 26, wherein said polypeptide stimulates T cell proliferation.

213. The polynucleotide of claim 212, wherein the sequence of said amino acid sequence is at least 95% identical to amino acids -38 to 245 of SEQ ID NO:26.

214. A method of producing a vector which comprises inserting the polynucleotide of claim 212 into a vector.

215. A vector comprising the polynucleotide of claim 212.

216. A host cell comprising the polynucleotide of claim 212 operably associated with a heterologous regulatory element.

217. A method of producing a polypeptide which comprises culturing the host cell of claim 216 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

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218. An isolated polynucleotide comprising a nucleic acid encoding amino acids 1 to 245 of SEQ ID NO:26.

219. The polynucleotide of claim 218, comprising nucleotides 123 to 857 of SEQ ID NO:25.

220. The polynucleotide of claim 218, comprising a nucleic acid encoding amino acids -38 to 245 of SEQ ID NO:26.

221. The polynucleotide of claim 220, comprising nucleotides 9 to 857 of SEQ ID NO:25.

222. A method of producing a vector which comprises inserting the polynucleotide of claim 218 into a vector.

223. A vector comprising the polynucleotide of claim 218.

224. A host cell comprising the polynucleotide of claim 218 operably associated with a heterologous regulatory element.

225. A method of producing a polypeptide which comprises culturing the host cell of claim 224 under conditions such that said polypeptide is expressed, and recovering said polypeptide.--

226. (new) An isolated polynucleotide comprising a nucleic acid encoding a polypeptide comprising 30 contiguous amino acids of the amino acid sequence of SE ID NO: 26, wherein said 30 contiguous amino acids comprises an antigenic determinant for the polypeptide consisting of the amino acid sequence of SEQ ID NO: 26.

227. (new) A method of producing a vector which comprises inserting the polynucleotide of claim 226 into a vector.

228. (new) A vector comprising the polynucleotide of claim 226.

229. (new) A host cell comprising the polynucleotide of claim 226 operably associated with a heterologous regulatory element.

230. (new) A method of producing a polypeptide which comprises culturing the host cell of claim 229 under conditions such that said polypeptide is expressed, and recovering said polypeptide.

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